

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 145765

TO: Terry McKelvey

Location: REM-2A75&2C70

Art Unit: 1636

Saturday, March 05, 2005

Case Serial Number: 10/006116

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner McKelvey,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527





Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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061955; GB:D30785; NID:g1648847; PIDN:BAA06451.1; PID in homology plogy <try></try>	cule type: mRNA dues: 1-260 <res> s-references: UNIPROT:Q61955; GB:D30785; rfamily: trypsin; trypsin homology 52/Domain: trypsin homology <try></try></res>	A,Molecule A,Residues A,Cross-re C,Superfam F,33-252/D	ycin I s cal prot (EC 3.4 ein - Pa chain V		2591 2591 2375 43	, , , , , , , , , , , , , , , , , , ,	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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241 IRMIMRN 247 : 252 IKKTMDN 258	181 TSNMVCAGGVPGQDACQGDSGGP 193 TEGMVCAGSSNGADTCQGDSGGP	121 TSSVQPLFLPNDCATAGTECHVS(- - - - - - - - - - - - - - - - - - -	62 HCSGSRYWVRLGEHSLSQLDWTE : : 73 HCKKQKYSVRLGDHSLQSRDQPE	Local S nes 121 5	62 4.5 552 2 662 4.5 566 2 4.5 662 4.5 666 2 4.5 666 2 4.5 666 2 4.5 666 2 4.5 662 4.5 662 4.5 662 4.5 662 4.5 662 4.5 662 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 4.5 663 2 162 62 4.5 693 2 162 62 4.5 693 2 162 62 62 62 62 62 62 62 62 62 62 62 62 6
	TSNNVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 	TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI : : -	HCSGSRYWVRLGEHSLSQLDWTBQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV	imilarity 49.0%; Pred. No. 3.2e-43; ; Conservative 28; Mismatches 93; Indels 5; Gaps ; FLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA	MENTS ME
	VYTYICKYVDW 240 : VYTKICRYTTW 251	ATCHGVYPGRI 180 : NKCERAYPGKI 192	RLLRLRUPVRV 120 : : MLIRLQNSANL 132	5; Gaps 3; LIDHRWVLTAA 61 : LVGDRWVLTAA 72	hypothetical prote hemagglutinin prec hydrogenase-2 larg hydrogenase-2 larg hydrogenase-2 larg epithelin/granulin hypothetical glyci protein kinase C (hypothetical prote prose protein [impo death receptor-6- zinc finger protei translational elon ; Tanaka, T.; Ito, J.; Nishing el limbic-serine protease genu el limbic-serine protease genu el limbic-serine protease genu

proteinase; zymogen

12;

Gaps

59

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A;Residues: 1-248 <WAN1>
A;Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NII
A;Experimental source: clone 1-938
A;Accession: $72345
A;Molecule type: DNA
A;Residues: 1-248 <WAN2>
A;Accession: $2065
A;Accession: $5065
A;Accession: $55065
A;Molecule type: mRNA
A;Accession: $55065
A;Molecule type: mRNA
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248 <WAN3>
A;Cross-references: EMBL:U15155; NID:g603902; PIDN:AAA79912.1; PID:gAccession: $72346
A;Accession: $72346
                submitted to the EMBL Data Library, A;Reference number: $71155
                                                                                 A;Molecule type: DNA
A;Residues: 1-9,'V',11-12,'T',14-102,'A',104-214,'I',216-248
A;Cross-references: GB:U15155; NID:g603902; PIDN:AAA79912.1;
A;Experimental source: clone P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NiAlternate names: trypsinogen I
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S55067; S72345; S55065; S72346; S71155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A; Title: Isolation and characterization of
A; Reference number: S55065; MUID: 95251611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-248 < WAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trypsin (EC 3.4.21.4) I precursor, pancreatic -
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C. Superfamily: trypsin tomology
C. Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;11-16/Domain: signal sequence #status predicted <SIG>
F;17-25/Domain: activation peptide #status predicted <APT>
F;26-248/Product: trypsin II #status predicted <APT>
F;26-241/Domain: trypsin homology <TRY>
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A;Experimental source: clone 2-P29
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A;Experimental source: clone 2-p29
A;Accession: S72347
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWIQ 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITSNWICVGFLEGGKDSCQGDSGGPVVCNGELQGIVSWG-IG-CALKGYPGVYTKVCNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITSNMVCAGGVP-GODACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAHCYKSRIQVRLGEYNIDVQEDSEVVRSSSVIIRHPKY--SSITLNNDIMLIKLASAVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFLTLSCLGAAVAFPGGADDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGSLINSQWVLS
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47.5%; Pred. No. 6e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Mismatches
                                        September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIPROT: Q90628; EMBL: U15156; NID: g603904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g6039
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                                                                                                            PID:g603903
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                                                                                   A;Note: at position 20, Ile and Val occur alternatively ()Superfamily: trypsin; trypsin homology C;Neywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; p:1-231/Product: trypsinogen #status experimental <ZYM>F;1-231/Product: trypsinogen #status experimental <APT>F;9-231/Product: trypsin #status experimental <APT>F;9-231/Product: trypsin #status experimental <AMT>F;9-231/Product: trypsin homology <TRY>F;9-224/Domain: trypsin homology <TRY>F;9-224/Domain: trypsin homology <TRY>F;15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted F:48,92,185/Active site: His, Asp, Ser #status predicted P:48,92,185/Active site: His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 9-231 < HER>
                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Determination of the amino acid sequence of porcine A;Reference number: A90368; MUID:73258692; PMID:4738933 A;Accession: A90368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 69, 1
A;Title: Su le trypsinogene
A;Reference number: A90641
                                                                      F;60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P00761
R;Hermodson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
Biochemistry 12, 3146-3153, 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
C;Accession: A90641; A90388; A00947
R;Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.
Biochim. Biophys. Acta 69, 115-129, 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-10 < CHA>
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C; Superfamily: trypsin; trypsin homology
C; Kuywords: hydrolase; pancreas; protein digestion; serine
F; 1-15/Domain: signal sequence #status predicted <APT>
F; 16-25/Domain: activation peptide #status predicted <APT>
F; 26-248/Product: trypsin I #status predicted <MAT>
F; 26-241/Domain: trypsin homology <TRY>
F; 26-241/Domain: trypsin homology <TRY>
F; 26-241/Domain: trypsin homology <TRY>
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A;Molecule type: mRNA
A;Residues: 1-102,'A',104-248 <WANS>
A;Cross-references: EMBL;U15156; NID:g603904; PIDN:AAA79913.1; PID:g603905
  Best Local Similarity
                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 VLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKFLVLVAFLGVAVAFPISDEDDDKIVGGYSCARSAAPYQVSLNSGYHF-CGGSLISSQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VISAAHCYKSSIQVKLGEYNLAAQDGSEQTISSSKVIRHSGY--NSNTLNNDIMLIKLSK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSIFILLCVIG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGRITSNMICIGYLNGGKDSCQGDSGGPVVCNGQLQGFVSWG-IG-CAQKGYPGVYTKVC
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  46.7%;
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45.5%; Pred. No. 9.6e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
  Score
Pred.
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     No.
2.7e-38;
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                                                                   Glu) #status predicted
                  Length 231;
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trypsin by sequenator

analys

proteinase;

09-Jul-2004

235

235

177 176

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C;Superfamily: trypsin; trypsin homology
C;Kupwords: hydrolase; protein digestion; serine proteinase
F;1-15/Domain: signal sequence #status predicted <SIG>F;16-20/Domain: activation peptide #status predicted <APT>F;21-236/Domain: trypsin homology <TRY>F;26-243/Product: trypsin I #status predicted <MAT>F;27-157,45-61,129-230,136-203,168-182/Disulfide bonds: #status predicted F;60,104,197/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog C;Species: Kenopus laevis (African clawed frog)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A35871; S12117
R;Shi, Y.B.; Brown, D.D.
Genes Dev. 4, 1107-1113, 1990
Genes Dev. 4, 1107-1113, 1990
A;Reference number: A35871; MUID:91007255; PMID:2210372
A;Accession: A35871
serine proteinase SCCE precursor -
N;Alternate names: stratum corneum
C;Species: Homo sapiens (man)
                                                          RESULT
A53968
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A; Residues: 1-243 < SHI>
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A35871
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Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                        RMIMRNN 248
                                                                                                                                                                                                                            NMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI 241
                                                                                                                                                                                                                                                                                                                      SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD
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                                                                                                                                                                                                                                                                                     AVNTVPLPSGCSAAGTSCLISGWGNTLSNGSNYPDLLQCLNAPILTNAQCNSAYPGEITA
                                                                                                                                                                                                                                                                                                                                                                CYKASIQVRLGEHNIALSEGTEQFISSSKVIRHSGY--NSYTLDNDIMLIKLSSPASLNA
                                                                                                                                                                                                                                                                                                                                                                                                   CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                        FLLLCVL-LGAAAAFDDDKIIGGATCAKSSVPYIVSLNSGYHF-CGGSLITNQWVVSAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
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                                                                                                                                                                                                             NMI CVGYMEGGKDSCQGDSGGPVVCNGQLQGVVSWGY--GCAMRNYPGVYTKVCNYNAWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLLLCVLGLSQAAT---PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                    ONTIAAN
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Pred. No. 8.8e-38;
                     chymotryptic
                                         human
                       enzyme
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-246 <STE>
A;Residues: 1-246 <STE>
A;Cross-references: UNIPROT:P07146; GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919
A;Cross-references: UNIPROT:P07146; GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-24/Droduct: trypsin #status predicted <MANT>
F;24-246/Product: trypsin homology <TRX>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;30,107,200/Active site: His, Asp, Ser #status predicted
F;377,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: B25528
R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A;Title: Sequence organisation and transcriptional regulation
A;Reference number: A93646; MUID:87066713; PMID:3641189
A;Accession: B25528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin (EC 3.4.21.4) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
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A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
C;Genetics:
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C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>
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Accession: A53968
                                                                                                                                                                               Query Match
Best Local
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                                                                      LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
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MSALLILALVGAAVAFPVDDDDKIVGGYTCRESSVPYQVSLNAGYHF-CGGSLINDQWVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKVYKDLLENSMLCA-GIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTF-PCGQPNDPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTOVCKFTKWINDTMKKH
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Pred. No. 9.2e-38;
                                                                                                                                        Score 553; DB 2;
Pred. No. 1.3e-37;
5; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Nimbur, m.; starwayer, r.;

J. Moll. Biol. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution A;Reference number: A92954; MUID:76072997; MUID:512

A;Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C;Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a termi specudotrypsin. A cleavage may also occur after Arg-105.

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen f;1-229/Product: trypsinogen #status experimental <ZYM>
F;1-229/Product: trypsin bomology <TRY>
F;7-222/Domain: activation peptide #status experimental <APT>
F;6-7/Cleavage site: Lys-11e (enteropeptidase) #status experimental f;13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental F;58,60,63,68/Binding site: calcium (Glu, Ann, Val, Glu) #status experimental F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Contains: trypsinogen
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Appr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997
C;Accession: A90164; A00946; S08774
R;Mikes, O: Holeysovsky, V:; Tomasek, V:; Sorm, F.
Biochem. Biophys. Res. Commun. 24, 346-352, 1966
A;Title: Covalent structure of bovine trypsinogen. The position of the rema A;Reference number: A90164; MUID:67168848; PMID:5967094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: annotation; revisions
R; Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh,
Biochemistry 14, 1358-1366, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-57,70',59
R;Hartley, B.S.
Philos. Trans. R. Soc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: the sequence agrees with that shown R;Bode, W.; Schwager, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A93755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsin (EC 3.4.21.4) precursor - N;Contains: trypsinogen
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                      106;
                                         81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQFLFLPNDCATAGTEC 140
                                                                                                                                        21 KIFNGTECGRNSOPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
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EGNEQFISASKSIVHPSY--NSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQC
                                                                                          KIVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVV
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                                                                                                                                                                                              40.2%; Score 552; DB 1;
46.3%; Pred. No. 1.4e-37;
tive 40; Mismatches 77
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                                                                                                                                                                                                                                            Length 229
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C;Keywords: hyur---
F;24-239/Domain: trypsin homoroyy --
F;63,107,200/Active site: His, Asp,
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Eur. J. Biochem. 193, 767-773, 1990
A;Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anionic A;Reference number: S13813; MUID:91065383; PMID:1701147
A;Accession: S13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-247 <HUE>
A;Cross_references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:g830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trypsin (EC 3.4.21.4) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Dec-193 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S13813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
240
                                                                                                                                          183
                                                                                                                                                                                   122 RVSTLLLPSACASAGTECLISGWGNTLSSGVNYPDLLQCLVAPLLSHADCEASYPGQITN
                                                                                              182
                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                     64 CYQYHIQVRLGEYNIDVLEGGEQFIDASKIIRHPKY--SSWTLDNDILLIKLSTPAVINA
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                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                           RMIMRNN 248
                                                                                                                NMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGJPGVYTYICKYVDWI 241
                                                                                                                                                                                                                            SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
QETIAAN 246
                                                                                         NMICAGFLEGGKDSCQGDSGGPVACNGQLQGIVSWGY--GCAQKGKPGVYTKVCNYVDWI
                                                                                                                                                                                                                                                                                                                                   CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS
                                                                                                                                                                                                                                                                                                                                                                                      LILAFVGAAVAFPSDDDDKÍVGGYTCAENSVÞYQVSLNAGYHF-CGGSLINDQWVVSAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGPVVCSGKLQGIVSWGS--GCAQKNKPGVYTKVCNYVSWIKQTIASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIŚĠWĠNTKSSGTSYPDVĹKĊĹKAPILŚDSSĊKSAYPĠQITŚNMFĊAĠYLEGĠKDSCQĠD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%; Score 550; DB 2; Length 45.7%; Pred. No. 2.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                       239
                                                                                                                                                                                      181
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trypsin (EC 3.4.21.4) precursor, anionic - N;Alternate names: cationic trypsinogen C;Species: Canis lupus familiaris (dog) C;Date: 30-Sep-1987 #sequence_revision 30dog

30-Sep-1987 #text_change 09-Jul-2004

C;Accession: A26273
R;Pinsky, S.D.; LaFozge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation:
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Accession: A26273

full-length

mRNA

A;Molecule type: mRNA A;Residues: 1-247 <PINA A;Residues: 1-247 <PINA A;Cross-references: UNIPROT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095 C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen F;1-15/Domain: signal sequence #status predicted <SIG>

```
trypsin (EC 3.4.21.4) precursor, cationic - dog
N,Alternate names: cationic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Species: Ocanis lupus familiaris (dog)
C;Species: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: B26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
MO1. Cell. Biol. 5, 2669-2676, 1985
NO1. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Accession: B26273
A;Molecule type: mRNA
A;Residues: 1-246 <PINN
A;Cross-references: UNIPROT:P06871; GB:M11590; NID:g164096; PIDN:AAA30900.1; PID:g164097
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;16-15/Domain: activation peptide #scatus predicted <APT>
F;24-246/Product: trypsin homology <TRY>
F;24-239/Omain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,717-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
TRDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;16-23/Domain: activation peptide #status predicted <APT>
F;24-247/Product: trypsin, anionic #status predicted <ENZ>
F;24-239/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted F;30-160,48-64,132-233,139-206, 171-185/Disulfide bonds: #status predicted F;63,107,200/Active site: His, Asp, Ser #status predicted F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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Best Local S
Matches 111
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Best Local Similarity
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118
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                                        119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113;
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                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LILAFLG-AAVATPTDDDDKIVGGYTCEENSVPYQVSLNAGYHF-CGGSLISDQWVVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLCVLGLSQAATP-----KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
                                                                                                                                                                            MKTFIFLALLGATVÁFFIDDDDKÍVGGYTCSRNSVFYQVSLNSGYHF-CGGSLÍNSQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRMIMRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARVATISLPRACAAPGTQCLISGWGNTLSSGTNYPELLQCLDAPILTQAQCEASYPGQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCYKŚRIQVRLGEYNIDVLEGNEQFINŚAKVIRHPNY--NSWILDNDIMLIKLSSPAVLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVT 121
TLNSRVSAIALPKSCPAAGTQCLISGWGNTQSIGQNYPDVLQCLKAPILSDSVCRNAYPG
                                                                                                                               TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
                                                                                                                                                                                                                    LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENMICAGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGY--GCAQKNKPGVYTKVCNFVDW
                                                                                     SAAHCYKSRIQVRLGEYNIAVSEGGEQFINAAKIIRHPRY-NANTI-DNDIMLIKLSSPA
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248
                                                                                                                                                                                                                                                                                       39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.7%;
                                                                                                                                                                                                                                                                    43;
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                                                                                                                                                                                                                                                                 Score 545; DB 1;
Pred. No. 5.8e-37;
43; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 546; DB 1; Length 247; Pred. No. 4.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                              Length 246;
                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                 Gaps
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  177
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                                                                                                                                                                                                                  trypsin (EC 3.4.21.4) I precursor - rat N;Alternate names: trypsinogen I C;Species: Rattus norvegicus (Norway rat C;Date: 17-Dec-1982 #sequence_revision I C;Accession: B22657; A00948
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A;Molecule type: mRNA
A;Residues: 1-247 <FLE>
A;Cross-references: UNIPROT:P08426; GB:M16624; NID:g206498; PIDN:AAA41985.1;
A;Cross-references: UNIPROT:P08426; GB:M16624; NID:g206498; PIDN:AAA41985.1;
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology <TRY>
F;25-240/Domain: trypsin homology <TRY>
F;31-161,49-65,113-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;64,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trypsin (EC 3.4.21.4) precursor, cationic - rat cyspecies: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Aate: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_ch C;Aates: 30-Jun-1988 #text_ch C;Accession: A27547 R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C. Biochemistry 26, 3081-3086, 1987 A;Celesion: A27547; MUID:87271609; PMID:3607011 A;Accession: A27547; MUID:87271609; PMID:3607011 A;Accession: A27547; MUID:87271609; PMID:3607011
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RESULT 13
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                                                                                                                                  237
                                                                                                                                                                                                                                                                                                                                                                                                     60 VSAAHCYKSRIQVRLGEHNIDVVEGGEQFIDAAKIIRHPSY--NANTFDNDIMLIKLNSP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSIFLLLCVLGLSQAA----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV
                                                                                                                                                                                       GKITSNMFCLGFLEGGKDSCQGDSGGPVVCNGQLQGVVSWGY--GCAQKGKPGVYTKVCN 235
                                                                                                                                                                                                                            GRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICK 236
                                                                                                                                                                                                                                                                                                                                                VRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKALIFLAFLGAAVALPLDDDDDKÍVGGYTCQKNSLÞYQVSLNAGYHF-CGGSLÍNSQWV 59
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                                                                                   NAMIQQIVAAN
                                                                                                                                  YVDWIRMIMRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 544.5; DB 2;
Pred. No. 6.3e-37;
3; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-Jun-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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A;Molecule type: DNA
A;Residues: 1-246 <CRA>
A;Residues: 1-246 <CRA>
A;Cross-references: UNIPROT:P00762; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A;Cross-references: UNIPROT:P00762; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17:
R;MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: B22657; A00948
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
A;Accession: B22657
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Rutter,

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A;Cross-references: UNIPROT:P35033; EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388 C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; serine proteinase F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>F;8-15/Domain: activation peptide #status predicted <APT>F;16-238/Product: trypsin III #status predicted <WAT>F;16-238/Product: trypsin homology <TRY>F;16-231/Domain: trypsin homology <TRY>F;16-231/Domain: trypsin homology <TRY>F;22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted F;25-99,192/Active site: His, Asp, Ser #status predicted
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A;Reference number: i
A;Recession: A00948
A;Molecule type: mRNJ
A;Residues: 1-246 <MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
S31779
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-238 < MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <APT>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-246/Product: trypsin I #status predicted <ENZ>
F;24-245/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;33,107,200/Active site: His, Asp, Ser #status predicted
F;63,77,80,85/Binding site: calcium (Giu, Asn, Val, Giu) #status predicted
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                                                                                                                      Matches
                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
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KIVGGYECRKNSASYQASIQSGYHF-CGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVN 73
                                                KIENGTECGRNSQEWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGEITSSMICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWGY--GCALPDNPGVYTKVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGRITSNWVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGFCGQDGIFGVYTYIC 235
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                                                                                                        39.3%; Score 540; Di
47.2%; Pred. No. 1.4,
tive 37; Mismatches
                                                                                                           9 540; DB 2; I
No. 1.4e-36;
smatches 78;
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S05494
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A;Tille: A fourth trypsinogen (P23) in the rat pancreas induced by CCK A;Reference number: S05494; MUID:89386010; PMID:2780302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypsin (EC 3.4.21.4) IV precursor - rat
N;Alternate names: 23K protein; trypsinogen IV precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S05494
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237
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                                                                                                                                                                                                                                                                                                                                       59 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
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LSWIQETMANN
                                            VDWIRMIMRNN 248
                                                                                                                 RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY 237
                                                                                                                                                                                                                                                                                             SAAHCYKRKLOVRLGEHNIHVLEGGEOFIDAEKIIRHPEY--NKDTLDNDIMLIKLKSPA 118
                                                                                                                                                                                                                                                                                                                                                                                       MKISIFFAFLGAAVALPVNDDDKIVGGYTCPKHLVPYQVSLHDGISHQCGGSLISDQWVL
                                                                                         QÍTSNMFCLGFLEGGKDSCDGDSGGÞVVCNGEIQGIVSWGSV--CAMRGKÞGVYTKVCNY 236
                                                                                                                                                                                           VLNSQVSTVSLPRSCASTDAQCLVSGWGNTVSIGGKYPALLQCLEAPVLSASSCKKSYPG
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43.4%; Pred. No. 4.9
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Search completed: March 5, 2005, 18:17:26
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Result
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is derived by analysis of the total score distribution.
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1374
1 MGLSIFLLLCVLGLSQ:
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2: uniprot_trembl:*
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Q61S10
KKF HUMAN
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CHICK
KLKE HUMAN
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"The secreted protein discovery initiative (SPDI), a large-scale RT effort to identify novel human secreted and transmembrane proteins: a RT bioinformatics assessment."; RL Genome Res. 13:2265-2270(2003). RN [5] RP SEQUENCE FROM N.A. PubMed=15057824; DOI=10.1038/nature02399; RX Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., RA Carneped J., Gordon L.A., Grimwood J., Gordon L.A., Charnet D., Couronne O., Tran-Gyamfi M., RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C., RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,	Gene 2 [4] SEQUEN MEDLIN Clark Chen J Eaton Huang Lewis Seshag Vandle Yi S Godows	RN SEQUENCE FROM N.A. (ISOFORM 1). RY SEQUENCE FROM N.A. (ISOFORM 1). RX MEDILINE=20118156; PubMed=10652563; RA Yousef G.M., Luo LY., Diamandis E.P.; RT Yousef G.M., Luo LY., Diamandis E.P.; RT 19q13.3-q13.4."; RI 19q13.3-q13.4."; RL Anticancer Res. 19:2843-2852(1999). RN [2] RN [2] RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). RA SOUSEG G.M., Magklara A., Scorilas A., Diamandis E.P.; ROUSEG G.M., Magklara A., Scorilas A., Diamandis E.P.; RL Scoulact FROM N.A. (ISOFORM 1). RA SEQUENCE FROM N.A. (ISOFORM 1). RA Moss P., Paeper B., Wang K.; RA Moss P., Paeper B., Wang K.; RT Cluster located in chromosome 19q13 region.";	RESULT 1 KLKC HUMAN STANDARD; PRT; 248 AA. AC Q9UKRO, Q9UKRI; DT 16-OCT-2001 (Rel. 40, Created) DT 16-OCT-2004 (Rel. 45, Last sequence update) DT 25-OCT-2004 (Rel. 45, Last annotation update) DT Xallikrein 12 precursor (EC 3.4.21) (Kallikrein-like protein 5) DE KALLS) (UNG669/PRO1303). GN Name=KLKL1; Synonyms=KLKL5; OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. OK NCBI_TaxID=9606;	1492 248 18.0 374 2 Q80YD5 Q80yd5 mus musculu 1493 248 18.0 392 2 Q9YWZ3 Q9YmZ3 drosophila 1494 248 18.0 401 2 Q6LHI7 Q6LHI7 photobacter 1495 247.5 18.0 250 2 Q9U414 Q9u4i4 plodia inte 1496 247.5 18.0 291 2 Q6Y1Y9 Q6Y1Y9 1 you sline 1497 247 18.0 293 2 Q708413 Q6Y1Y9 lygus line 1498 247 18.0 243 2 Q708Q5 Q708Q5 Q708Q5 anopheles g 1499 247 18.0 350 2 Q9VZJ9 Q9vCJ9 drosophila 1500 247 18.0 350 2 Q9WIX6 Q9wIX6 drosophila

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A Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
A Rodriguez M., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
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O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310008B01 product:similar to KALLIKREIN 12 (EC 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
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          SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE=Tongue;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

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the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome
60,770 full-length cDNAs.";
Nature 420:563-573(2002)
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STRAIN=C57BL/6J; TISSUE=Tongue;
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STRAIN=C57BL/60; TISSUB=Tongue;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
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STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1374;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                    h Group
based c
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse
                                                                                                                                                                                                                                                                                    p Phase I & II
on functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA collection.";
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                                                                                                                                                                                                                                                                                  Team; annotation
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                                                          6
                                   genes.";
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Tagami M., Shibata Y., Sh.

Lagami M., Tagawa A., Tak

Lagami M., Yamamura T., Yasunishi A., Yasunishi A., Yamamura T., Yasunishi A., Yasunishi A.
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Best Local (
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF000089; Trypsin; 1.
PRINTS; PR000920; Trypsin; 1.
RRINTS; PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS0134; TRYPSIN_DSM; 1.
PROSITE; PS0134; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CC7BL/GJ; TISSUE=Tongue;
STRAIN-CC7BL/GJ; TISSUE=Tongue;
Adachi J., Alzawa K., Akahira S., Pukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagaha A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINB-20530913, PubMed-11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshika M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Protease; Serine protease, NON TER 1 1 1 SEQUENCE 234 AA; 25888 MW; 6D81E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=C57BL/6J; 7
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                                                                                                                                                ATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQ 193
                                                                                                                                                                                                                                                                                                                                                                                              LSQAATFKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLG
                                                                                                                                                                                                                                                                          EHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDC
                                                                                                                                                                                                                                                                                                                                                                  LSQADREKIYNGVECVKNSQPWQVGLFHGKYLRCGGVLVDRKWVLTAAHCR-DKYVVRLG
DACQGDSGGPLVCGGVLQGLVSWGSVGPCGQKGIPGVYTKVCKYTDWIRIVIRNN
                                                                                                                                                                                                                              HILLIFF THE SYCHAYONHEHDLRLIRLINR PIHLTRAVR PVALPSSC
                                                           DACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN
                                                                                                                   VTTGAMCHVSGWGTTNKPWDPFPDRLQCLNLSTVSNETCRAVFPGRVTENMLCAGGEAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 952.5; | Pred. No. 1.9e 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6D81E609EDD39110 CRC64;
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RESULT 3 KLK8_HUMAN

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SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=22807296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.

Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagits A.,

Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Vansura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

Godowski P., Gray A.,

The George T. School Covery initiative (Spin) a large scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien T.J.; "Cloning of tumor-associated differentially expressed serine protease overexpressed by ovarian carcinoma."; Cancer Res. 59:4435-4439(1999).
SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
Lamerdin J.E., MCCready P.M., Skowronski E., Visw
Burkhart-Schultz K., Gordon L., Dias J., Ramirez
Phan H., Velasco N., Do L., Regala W., Terry A.,
                                                                                         "The secreted protein discovery effort to identify novel human s bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., Moss P., Paeper B., Wang K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).

Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;

"Molecular cloning and characterization of a novel serine protovasin, a potential molecular marker for ovarian carcinomas.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitsui S., Tsuruoka N., Yamashiro "A novel form of human neuropsin, generated by alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein protease TADG-14) (Tumor-associated differentially protein) (UNQ283/PRO322).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLK8_HUMAN STANDARD; PRT; 260 AA.
060259; 09HCB3; Q9UIL9; Q9UQ47;
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     generated by alternative
human adult brain.";
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MEDLINE=98372070; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=KLK8; Synonyms=NRPN, PRSS19, Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                  Gene
                                                                                                                                                                                                                                                                                                                                                                                                 "Sequencing and expression analysis of the serine protease cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99413504; PubMed=
Underwood L.J., Tanimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98372070; PubMed=9714609; DOI=10.1016/S0378-1119(98)00232-7;
Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
"Sequence analysis and expression of human neuropsin cDNA and gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                    257:119-130(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10485494;
**rimoto H., Wang Y., Shigemasa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260:627-634 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10102990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM 1)
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                                                                                                                             initiative (SPDI), a large secreted and transmembrane
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a brain-related serine protease,
and is expressed preferentially
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Viswanathan V.,
irez M., Stilwagen
A., Brower A., Ga
                                                                                                                                               a large-scale
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                                                                                                                             proteins:
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     Garnes
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RASE REPRESENTATION OF THE PROPERTY OF THE PRO
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EMBL; AB012761; BAA88684.1; -
EMBL; AB010780; BAA88684.1; -
EMBL; AB008390; BAA82665.1; -
EMBL; AB008927; BAA82666.1; -
EMBL; AF055982; AAD56050.1; -
EMBL; AF095742; AAD25979.1; -
EMBL; AF095743; AAD25974.1; -
EMBL; AF043527; AAG233361.1; -
EMBL; AF243527; AAG33361.1; -
EMBL; AF243527; AAG33351.1; -
EMBL; AF243527; AAG33351.1; -
EMBL; AF243527; AAG33351.1; -
EMBL; AF243527; AAG33354.1; -
EMBL; AF243527; AAG33354.1; -
EMBL; AF243527; AAG33354.1; -
EMBL; AF243527; AAG33354.1; -
EMBL; AF243527; AAG33254.1; -
EMBL; AF24567; EMBL; AF24567; AF2567; AF2
            SIGNAL
SIGNAL
PROPER
CHAIN
ACT SITE
ACT SITE
ACT SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; Trypsin; 1.

PRINTS; PR00772; CHYMOTRYPSIN.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0008236; F:serine-type peptidase GO; GO:0007399; P:neurogenesis; TAS. InterPro; IPRO09003; Pept Ser Cys. InterPro; IPR001254; Peptidase S1. InterPro; IPR001314; Peptidase S1A. Dfsm. DFn00000
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MH,
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: Suggested to be involved in kindling epileptogenesis hippocampal plasticity.
-i-CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
-i-SUBCELLULAR LOCATION: Secreted.
-i-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller I Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi Jolsen A.S., Carrano A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId-060259-2; Sequence=VSP 005401; TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in pancreas while isoform 2 is expressed in adult brain and hippocampus. Both forms are also found in fetal brain and placenta. Not detected in kidney, spleen, liver and lung. SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
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            splicing;
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   Potential.
By similarity.
Neuropsin.
Charge relay sy
Charge relay sy
Charge relay sy
By similarity.
N-linked (Glona)
A -> AACGSLDLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !!!!!!!!!!!!
nked (GlcNAc. . .) (Potential).
AACGSLDLLTKLYAENLPCVHLNPQWPSQPSHCPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity; TAS
                                                                                                                                                                                                                                 system system
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are no restrictions
its content is in
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.R.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.R.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Jordan H., Moore T., Ray S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Foters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,
RA Broak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Best Local S
Matches 123
Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; BC040887; AAH40887.1; -.
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HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia: Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                       SEQUENCE FROM
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01-MAR-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Kallikrein 8, isoform 1
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                                                                                                                ISSUE=Brain;
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                                                                                                                                                                                                                          sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12477932; DOI=10.1073/pnas.242603899; Feingold E.A., Grouse L.H., Derge J.G.,
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/FTId=VSP_005401.
EF439E5B8C83E660 CRC64;
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GO; GO:0004263; F:chymotrypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IE;

R InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

PR InterPro; IPR0031; Pept Ser Cys.

PRAMT; PR00089; Trypsin; 1.

PR PAMRT; SM00072; CHYMOTRYPSIN.

DR PROSITE; PS50240; TRYPSIN DOM; 1.

DR PROSITE; PS50240; TRYPSIN HIS; UNKNOWN 1.

DR PROSITE; PS00134; TRYPSIN SER; 1.

KW Hydrolase; Protease; Serine protease.

Hydrolase; Protease; Serine protease.
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Best Local Similarity
Matches 123; Conserv
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Q61955;
                                                                                                                   SEQUENCE FROM N.A.

STRAIN-BALB/C, TISSUE=Hippocampus;

MEDLINE=95348817; PubMed=7623137;

Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki
Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka
"Expression and activity-dependent changes of a nov
protease gene in the hippocampus.";

J. Neurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein Name=Kkk8; Synonyms=Nrpn, Prss19;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
 STRAIN=Czech II;
            SEQUENCE FROM
                                        Submitted
                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                Yoshida S.,
                                                                                           SEQUENCE FROM
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Hirata A.,
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TISSUE-Mammary gland
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28090 MW; EF5934EB96295660 CRC64;
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50.2%; Pred. No. 2.26
tive 24; Mismatches
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                                        the
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                                        EMBL/GenBank/DDBJ
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                                                              Shiosaka S.;
neuropsin gene,
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MEROPS; S01.244; -. MGD; MGI:892018; Klk8

IPR009003;

Pept_Ser_Cys

1NPM; X-ray; A/B=33-256

I56559

PIR; 156559;

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rohas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahards S. Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human remember and mouse Change Company of the company of the company of than 15,000 full-length human remember and mouse Change 
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE=Brain; MEDLINS=98255202; PubMed=955608; DOI=10.1074/jbc.273.18.11189; Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumo Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.; "Characterization of recombinant and brain neuropsin, a plastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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J. Biol. Chem. 273:11189-11196(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF N-TERMINUS, CHARACTERIZATION,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE=Ref.4.
MASS SPECTRON
NOTE=Ref.4.
SIMILARITY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Expressed specifically in the limbic mouse brain and is localized at highest concentration in neurons of the hippocampal CA1-3 subfields.

MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Preferential cleavage: ENZYME REGULATION: Strongly inhibited by d: fluorophosphate, leupeptin and (4-amidinophosphate)
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D30785; BAA06451.1; -.
AB032202; BAA92435.1; -.
BC055895; AAH55895.1; -.
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PRINTS; PRO0722; CHYMOTRYPSIN.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

3D-structure; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                  Serine protease;
                                                                                                                                                                                                                                                                                                                                                                         InterPro;
    62
              13
                       v
                                       Similarity
 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV
           ILLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWVLTAA
                     IFLLLCV----LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                                                                                                                                                                                                  IPR001254; Peptidase S1.
IPR001314; Peptidase S1A.
                                 Conservative
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Potential.
                                 28;
                                Score 622.5;
Pred. No. 5.6e
28; Mismatches
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRALN=Fischer; TISSUE=Brain;

RC STRALN=Fischer; TISSUE=Brain;

RX MEDLINE=98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;

RA Davies B.U., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;

RT "Serine proteases in rodent hippocampus.";

RL J. Biol. Chem. 273:23004-23011(1998).

CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and CC hippocampal plasticity. Has a strong proteolytic activity against CC fibronectin (By similarity).

CC -!- TISSUE SPECIFICITY: Perferential cleavage: Arg-, Lys-.

CC --- SUBCELLULAR LOCATION: Secreted (By similarity).

CC --- TISSUE SPECIFICITY: Restricted to hippocampus.

CC --- TISSUE SPECIFICITY: Restricted to hippocampus.
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O88780;
O88780;
I 15-JUL-1999 (Rel. 38, Created)
II 15-JUL-1999 (Rel. 38, Last sequence update)
II 25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kall)
                                                                                                                                                                                                    InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Glycoprotein; Hydrolase; Serine prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ005641; CAA06643.1; -. HSSP; Q61955; INPM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstations the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commence this requires a license agreement (See http://www.isb-sib.ch/annoventities requires a license agreement (See http://www.isb-sib.ch/annoventities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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By similarity.
Neuropsin.
Charge relay system
Charge relay system
Charge relay system
                                                                                                                                                                            Potential.
                                                                                                                                                                                                    protease; Signal;
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  (See http://www.isb-sib.ch/announce/
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) (Kallikrein
   (By similarity).
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(By similarity).
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Q9UBX7; O75837; Q9S65;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 11 precursor (EC 3.4.21.-) (Hippostorotease) (UNQ649/PRO1279).

Name=KLK1; Synonyms=PRSS20, TLSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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DISULFID
CARBOHYD
                                                                                                                                                                                                                             TISSUE=Hippocampus;
MEDLINE=98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
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MEDLINE-20329229; PubMed=10872828; DOI=10.1006/bbrc.2000.2761;
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Biochem. Biophys. Res. Commun. 272:205-211(2000).
                                                                                         SEQUENCE FROM N.A.
MEDLINE-20130117; E
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                           63:88-96 (2000)
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 (ISOFORM 1)
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Pred. No. 6.7e-42;
                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                         DOI=10.1006/geno.1999.6072;
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(Hippostasin) (Trypsin-like
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AMEDINE-22388/57; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Ra Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rabieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rabieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rabieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rabieton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., An Halesley R.W., Touchman J.W., Green E.D., Dickeon M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and many servences".
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RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,

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Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

A Melson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

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Punacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,

Panacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903 (200: FUNCTION: Possible multifunctional protease. bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallil weakly cleaves other substrates for kallikref SUBCELLULAR LOCATION: Secreted.
                                                                                                                                    mouse cDNA sequences.";
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                                                                      99:16899-16903 (2002).
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kallikrein and
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                                                                                                                                                                  full-length human
                                                           substrate,
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                                                                                                                                                            MIN; 504434; ...

CO; GO:0008236; F:serine-type peptidase activity; TAS.

InterPro; IPR009003; Pept Ser Cys.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

R Pfam; PF00089; Trypsin; 1.

R PROSITE; PR00722; CHYMOTRYPSIN.

R PROSITE; PS50240; TRYPSIN DOM; 1.

R PROSITE; PS50213; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN ERR; 1.

R PROSITE; PS00135; TRYPSIN ERR; 1.
                                                                                Matches
                                                                                          Query Match
Best Local
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@eisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H-InvDB; HIX0015375; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.257; -. Genew; HGNC:6359; K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOId=Q9UBX7-2; Sequence=VSP 005402;
-I- TISSUE SPECIFICITY: Expressed in brain;
1 is expressed preferentially in brain;
-I- SIMILARITY: Belongs to the peptidase S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB012917; BAA33404.1; ALT INIT.

AB013730; BAA88713.1; ---

AB041036; BAA96797.1; ---

L; AF164623; AAD47815.1; ---

L; AF243527; AAG3364.1; ---

L; AC359014; AAG23257.1; ---

L; BC022068; AAH22068.1; ---

L; BC022068; AAH22068.1; ---
                                                                             120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
      63
                              4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9UBX7-1;
                                                                                          Similarity
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV
                      LQLILLALATGLVGGET-RIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
                                              LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                250
                                                                                                                              AA;
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                                                                                                                              27466
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                                                                                                                              MW;
                                                                            35;
                                                                                                                                                          By similarity.
N-linked (GlcNAc. . . ) (Potential).
N-linked (GlcNAc. . . ) (Potential).
N-linked (GlcNAc. . . ) (Potential).
N-linked (GlcNAc . . ) (Potential).
                                                                          Score 618.5;
Pred. No. 1.1e
35; Mismatches
                                                                                                                                        (in isoform /FTId=VSP_00
                                                                                                                                                                                                                                                                                                     Charge relay system Charge relay system Charge relay system
                                                                                                                                                                                                                                                                                                                                            Activation peptide Kallikrein 11.
                                                                                                                          TId=VSP_005402.
192D910BBCDC7A56 CRC64;
                                                                                     5; DB 1;
1.1e-41;
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89
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                                                                                                                                                                                                                                                                                                                                                         (Potential)
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(By similarity).
(By similarity).
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Q7JIG6
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Best Local S
Matches 118
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
SEQUENCE 255 AA; 28078 MW; A040914ABC8FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7JIG6
Q7JIG6;
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olsson Y., Persson M., Lundwall A.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: Belongs to peptidase family SI
EMBL; AF173845; AAS45302.1; -.
HSSP; P00761; lAKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080; Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundwall A.; "Glandular kallikreins of the cotton-top tamarin: molecular clonin the gene encoding the tissue kallikrein."; DNA Cell Biol. 19:721-727(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saguinus oedipus (Cotton-top tamarin).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P; P00761; IAKS.
GO:0004263; F:chymotrypsin activity; IEA.
GO:0008233; F:peptidase activity; IEA.
GO:0004295; F:trypsin activity; IEA.
GO:0004295; P:proteolysis and peptidolysis;
                                                             141
                                                                                                                                                                                                                                                                                                                  118;
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                             DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
VVSGWGLVSHNEPGTTGRPQSQVSLPDTLHCANISIISDASCDKNYPGRLTNTMVCAGAE
                                                  HVSGWGITNH-----PRN--PFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGV 190
                                                                                               DGPEQLRTASRVIPHPRY--EARSHRHDIMLLRLVQPARLTPQVRPVVLPTRCPHPGEAC
                                                                                                                                                                                                                                                  KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
                                                                                                                                                                                                  KLLEGEECAPHSQPWQVALYERGRFNCGASLISPHWVLSAAHCQSRFMRVRLGEHNLRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
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27,
27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                         A040914ABC8FEC8D CRC64;
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RESULT

ID 3272

AC Q63272

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AC Q6627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                               Q8CGR4;
Q8CGR4;
Q1-MAR-2003
01-MAR-2003
01-MAR-2004
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Q63ZF2;
25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                 Prostin.
Name=Klk15; Synonyms=KLK15;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordat;
Mammalia; Eutheria; Rodenti
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Olsson A.Y., Lilja H., Lundwall A.;
"Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen.";
Genomics 84:147-156(2004).
1- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
EMBL; BK001364; DAA05600.1; -.
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                                       NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
   SEQUENCE FROM N.A
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Rodentia;
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26,
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glandular kallikrein 11.
; 247B29D3F0DEF8F1 CRC64
                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
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PRINTS; PR0072; CHYMOTRYPSIN.
SMART; SM00020; Tryp SP0; 1.
PROSITE; PS50240; TRYPSIN DOM; 1
PROSITE; PS00134; TRYPSIN HIS; U
PROSITE; PS00135; TRYPSIN SER; U
PROSITE; PS00135; TRYPSIN SER; U
PROSITE; PS00136; TRYPSIN SER; U
PROSITE; PS0
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Q8IXD7;
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   Nakamura T., Mitsui
Submitted (JAN-2002)
                                                            TISSUE=Prostate;
                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                          SEQUENCE FROM N.A.
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
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       S.,
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Primates;
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   Miki
the 1
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Variant form hippostasin/KLK11.
Name=KLK11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2447533; Klk15.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006598; P:proteolysis and peptidolysis; IEA.
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i T., Yamaguchi N.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 608; DB 2;
Pred. No. 7.9e-41;
0; Mismatches 77
                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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  databases
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Best Local S
Matches 121
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6ISIO PRELIMINARY; PRT; 255 AA.
Q6ISIO; TOTAL CONTROL OF CONTROL 
                                                                                                                                                                                                                                                                                                  TISSUE=PCR rescued clones;
MEDLINE=22388257; PubMed 12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=KLKL5;
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
3L; AB078780;
3P; P00760; 1E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWGQ-DPCAITRKPGVYTKVCKYVDWIQETMKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHTLRCANITIIEHQKCENAYPGNITDTMVCASVQEGGKDSCQGDSGGPLVCNQSLQGII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQLILLALATGLVGGET-RIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.7%; Score 601; DB 2;
44.2%; Pred. No. 3.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT KLKF HU
ID KL
AC Q9
DT 16
DT 16
DT 25
DE KA
GN NA
GN NO
OC MA
OX NC
OX NC
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RN FI
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Best Local :
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InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR009003; Peptidase S1.
InterPro; IPR009003; Peptidase S1.
InterPro; IPR009003; Peptidase S1.
InterPro; IPR0090033; Peptidase S1.
InterPro; IPR0090033; Peptidase S1.
INTERPRO; INTERPRO
                                                                                                                                                                                                                   HUMAN STANDARD; PRT; 256 AA.

KKKF HUMAN STANDARD; PRT; 256 AA.

Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

25-OCT-2004 (Rel. 45, Last annotation update)

Kallikrein 15 precursor (EC 3.4.21.-) (ACO prote
  SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AN PubMed=11010966; DOI=10.1074/jbc.m005432200, Yousef G.M., Scorilas A., Jung K., Ashworth
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0004263; F:chymotrypsin activity; GO; GO:0004295; F:trypsin activity; IEA. GO; GO:0006508; P:proteolysis and peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Director MGC Project;
Submitted (APR-2004) to the
-!- SIMILARITY: Belongs to p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; ac.16902-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLTLSFLLASTAQDGDKLLEGDECAPHSQPWQVALYERGRFNCGASLISPHWVLSAAHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease; Serine protease
255 AA; 28016 MW; 1581B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.6%; Score 599; DB 2;
46.9%; Pred. No. 4.2e-40;
cive 32; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ d
peptidase family S1.
                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99:16899-16903 (2002) .
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(ACO protease).
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                                                    TISSUE SPECIFICITY.
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Schein J.E.,
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       E.P.;
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HSSP; P00760; 1EZX.

MEROPS; S01.081; -.

Genew; HGNC:20453; KLK15.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.

InterPro; IPR009003; Pept Ser Cys.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.
                                                                                                                                                                                                                    EMBL; AF242195; AAG09470.1; -.
EMBL; AF242195; AAG09470.1; -.
EMBL; AF242195; AAG09471.1; -.
EMBL; AF242195; AAG09472.1; -.
EMBL; AF243527; AAG33354.1; -.
EMBL; X75363; CAA53145.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                              entities
or send a
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J. Biol. Ch
   PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; TRYP_SPC; 1.
PROSITE; PSS0240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_IS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Мовв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S)
PubMed=14759258; DOI=10.1186/gb-2004-5-2-88;
Hillnan R. T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dihanich M.E., Spiess M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequencing and expression analysis cluster located in chromosome 19q13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94289486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                           e European Bioinformatics Institute. There are no restrictions on its e by non-profit institutions as long as its content is in no way diffied and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId-Q9H2R5-4; Sequence-VSP_005404; TISSUE SPECIFICITY: Highest expression in the thyroid glame expressed in the prostate, salivary, and adrenal glands and colon testis and kidney.

SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257:119-130(2000).
                                                                              PF00089; Trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9H2RS-2; Sequence=VSP 005405;
Note=May be produced at very low levels due to a premature codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9H2R5-3; Sequence=VSP_005406,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soId=Q9H2R5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biophys.
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Biophys. Acta 1218:225-228(1994).
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nem. 276:53-61(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOI=10.1016/S0378-1119(00)00382-6;
smith R., Argonza-Barrett R., Lei H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
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; FALSE_NEG.
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glands and
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Best Local S
Matches 121
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Q9QYN4;
01-MAY-2000
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SIGNAL
                                                                 MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2; Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.; "cDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the
-!- SIMILARITY: Belongs to
                                                                                                                                                                                           01-MAY-2000
01-MAR-2004
                           TISSUE=Brain;
                                       SEQUENCE
                                                                                                                   SEQUENCE
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                         Hippostasin.
Name=2310015I08Rik;
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                                      FROM N.A.
                                                         Biophys.
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                                                          Acta 1494:206-210(2000)
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Rodentia;
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13,
26,
           the EMBL/GenBank/DDBJ databases
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 peptidase
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                                                                                                                                                                                                              Created)
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Activation peptide (P
Kallikrein 15.
Charge relay system (
Charge relay system (
Charge relay system (
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2; Mismatches
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/FTId=VSP_005404.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_005407.
SHNEPGTAGSPRSQ ->
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                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599; DB 1;
No. 4.2e-40;
  family
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RESULT 15
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Q9QYN
DT Q1-MA
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OC Eukar
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RY MIDSI
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Matches 118
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GO; GO:0005615; C:extracellular space
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept Ser Cys.
Pfam; PF00089; Trypsin; 1.
PRLINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                            TISSUE=Prostate;
MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9QYN3
Q9QYN3;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hippostasin prostate type (Mus musculus adult male tongue cDNA, RI
full-length enriched library, clone:2310015108 product:protease,
serine, 20, full insert sequence) (Mus musculus adult male tongue
cDNA, RIKEN full-length enriched library, clone:2310040F07
product:protease, serine, 20, full insert sequence).
                                                   TISSUE=Prostate;
Yamaguchi N., Mitsui
                                                                                                                                                                     Mitsui S., Okui A., Kominami K., U
"cDNA cloning and tissue-specific
hippostasin/TLSP (PRSS20) ";
                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  product:protease, s
Name=2310015I08Rik;
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM;
PROSITE; PS00134; TRYPSIN HIS;
PROSITE; PS00135; TRYPSIN_SER;
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P00760; 1E
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                                                                                                                                                Biophys.
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249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;
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Pred. No. 5.
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A Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoka T., Hara K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Makai Y., Koido T., Owa C., Saito H., Saito R., Sakai K.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Shinagawa A., Shiraki T.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sagabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Sagabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Muramatsu M., Hayashizaki Y.,
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

2. ISIMILARITY: Belongs to peptidase family S1.

2. EMBL; AK009360; BAB26441.2; -.

2. EMBL; AK009720; BAB26441.2; -.

2. BEBL; AK009720; BAB26461.2; -.
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C STRAIN=C57BL/60; TISSUE=Tongue;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

X Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Hazama M., Nishine T., Harada A.,

X Konno H., Akiyama J., Nishi K., Kitsunai T., Tashire T., Harada A.,

X A Xonno H., Akiyama J., Nishi K., Kitsunai T., Kashiwagi K.,

X Yanamoto R., Matsunoto H., Sakaguchi S., Ikagami T., Kashiwagi K.,

X Yanamoto R., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Nokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

RI Genome Res. 10:1757-1771(2000).
                                                                        MGD; MGI:1929977; 2310015108Rik.
GO; GO:0005615; C:extracellular spa
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
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                           Pfam; PF00089; Trypsin; PRINTS; PR00722; CHYMOTI
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STRAIR-C57BL/60; TISSUE=Tongue;

MEDLINE=99279253; PubMed=10349636; DOI=10.10;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/60; TISSUE=Tongue;
MEDLINE=21085660; PubMed=1121/851;
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Nature 420:563-573(2002).
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P00760; 1E
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                                                                                                                                                                                           space;
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Search completed: March 5, 2005, 18:20:29 Job time : 178 secs
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1350 1351 1352 1353 1353 1354 1353 1354 1352 1355 1352 1356 132 1356 132 1357 132 1358 132 1359 132 1360 1361 1362 1363 1310.5 8.0 1363 130.5 8.0 1366 130.5 8.0 1366 130.5 8.0 1367 130.5 8.0 1368 130.5 8.0 1370 130.5 8.0 1371 1372 1372 1373 100.5 8.0 1374 1375 1376 105.5 7.7 1387 1387 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1388 105.5 7.7 1389 105.5 7 7 7 1389 105.5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	2 117.5 8.6 396 3 117.5 8.6 396 4 115.5 8.4 138 5 115.5 8.4 138 6 115 8.4 80 7 115 8.4 80 8 115 8.4 80 115 8.4 80 115 8.4 80

1125, App 125, App 125, App 125, App 125, App 144825, Ap 75, Appl 75, Appl

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US-09-012-692-77
PCT-USS5-14442A-77
PCT-USS5-14442A-77
US-08-906-769-101
US-08-907-95-101
US-08-907-95-101
US-08-907-95-101
US-08-906-613-101
US-08-906-613-99
US-08-906-613-99
US-08-906-613-99
US-08-906-613-99
US-08-906-613-99
US-08-906-613-13
US-08-908-909-10
US-08-18-913-14
US-09-106-468-14
US-09-106-468-14
US-09-106-468-14
US-09-106-468-14
US-09-270-767-32837
US-09-913-19191
 9-270-767-42857

8-293-778-11

9-270-767-32837

9-270-767-32837

9-252-991A-19191

9-911-842A-4

9-518-046-4

9-949-016-10403

9-949-016-10403

8-908-769-759783

8-906-767-59783

8-906-767-59783
Sequence
 77, Appl
77, Appl
77, Appl
77, Appl
101, Appl
102, Appl
103, Appl
104, Appl
105, Appl
106, Appl
107, Appl
108, Appl
109, Appl

                                                                                                                                                                                                                                                                                             Sequence 8151, Application US/09949016

Sequence 8151, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8151

LENGTH: 249

TYPE: PAT

ORGANISM: Human

US-09-949-016-8151
RESULT 2
US-09-999-016-6948
; Sequence 6948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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US-09-949-016-8151
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Best Local Similarity
Matches 247; Conserv
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                                                                                IRMIMRNN
                                                                                                                   TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                                                                    IRMIMRNN
                                                                                                        TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
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milarity 99.6%;
Conservative
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US-09-012-431-125

US-09-012-692-125

US-08-906-613-125

US-08-906-613-125

US-08-485-455D-75

US-08-485-455D-75

US-08-485-130C-75

US-08-484-211C-75

US-08-906-769-75

US-08-906-769-75

US-08-917-795-75

US-08-639-075A-75
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Pred. No. 3.1e
0; Mismatches
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}.1e-124;
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OF DETECTION AND
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                                                                                                                                                                                                                                                                            Length
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249; 1.

Gaps

241 240 181 180 121 120 62 60 USES

THEREOF

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APPLICANT: Ni, et al.

APPLICANT: Ni, et al.

FILE REFERENCE: PF391

CURRENT APPLICATION NUMBER: US/09/244,111

CURRENT FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 60/073,961

EARLIER APPLICATION NUMBER: 60/073,961

EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-244-111-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FBStSEQ for Windows Version 4.0
SEQ ID NO 6948
LENGTH: 254
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US-09-244-111-6
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; ORGANISM: Human
US-09-949-016-6948
                                                                                                                                                                           Query Match
Best Local
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Patent No. 6566498
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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                                                                          MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA 60
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                                                                                                                                                         Conservative
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                                                                                                                                                    Score 811; DB 4; Length 162; Pred. No. 3.8e-71; 0; Mismatches 3; Indels
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Sequence 7, Application US/09618259
Patent No. 6642013
GENERAL INFORMATION:
APPLICANT: O'Brien Timothy J.
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
FITLE OF INVENTION: No. 6642013e1 E.
FILE REFERENCE: D6020CIP2
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Sequence 2, Application US/09070526
Patent No. 6100059
GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: No. 6100059e1
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SEQ ID NO 7
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CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 260
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                       193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                     TDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW
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d, Lowell J.

6642013el Extracellular Serine Protease
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Pred. No. 2.5e-53;
4; Mismatches 93
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

Compounds

ADDRESSEE:

RATNER & PRESTIA

P.O.

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US-09-025-059-3; Sequence 3, Application US/09025059; Patent No. 6075136
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US-09-070-526-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                      GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA;
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for I
CURRENT APPLICATION DATA:
                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: VI
STATE: E
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 MFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAA 72
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Incyte Pharmaceuticals,
3174 Porter Dr.
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; CLONE: 1020091
US-09-025-059-3
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                                                                                                                                 Sequence 7, Application US/09008271A Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECHRONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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  TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 45.3%; al Similarity 49.0%; 121; Conservative 2
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  INVENTION: HUMAN PROTEASE MOLECULES
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                              Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
                    Tang,
Shah,
                                                                                                                 Hillman, Jennifer
                                                                                                                                                                                                                                                                                         258
                    Purvi
                                                                          Karl J.
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Pred. No. 1.5e-52;
28; Mismatches 93;
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Length 260; Indels

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Gaps

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72

93;

Indels Length

Gaps

192

251 240 132

72 61 w

260; 5

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RESULT 8
US-09-618-259-8
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                        GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine
FILE REFERENCE: D6020CIP2
                                                                                                                           Sequence 8, Application US/09618259
Patent No. 6642013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
          CURRENT APPLICATION NUMBER: US/09/618,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: COLNNOT27
CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheel
REGISTRATION NUMBER: 41,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 550-855-0555
                                                                                                                                                                                                                                                252
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                                                                                                                                                                                                                                                                                 241 IRMIM 245
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                                                                                                                                                                                                                                              IKKII 256
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TYPE: amino acid
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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ilarity 49.8%;
Conservative 2
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Pred. No. 1.5e-52;
14; Mismatches 94
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; PRIOR APPLICATION NUMBER: US 09
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: MUS SP.
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-618-259-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER APPLICATION NUMBER: 60/048,885
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
FILE REFERENCE: PZ007P1
FILE REFERENCE: PZ007P1
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ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,880
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,896
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-06-06
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                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
                                                                                                                                               APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
                  APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
                                                                                                               FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
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FILING DATE: 1997-06-06
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    APPLICATION
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49.0%;
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3ER: US 09
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Pred. No. 1.5e-52;
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DATE: 1997-12-18

**PLICATION NUMBER: 60/090,92

**PLICATION NUMBER: 60/092,921

**LER FILING DATE: 1998-07-15

**EARLIER APPLICATION NUMBER: 60/094,657

**EARLIER FILING DATE: 1998-07-30

**NUMBER OF SEQ ID NOS: 1227

**SOFTWARE: PATENTIAN Ver. 2.0

**SEQ ID NO 427

LENGTH: 250

TYPE: PRT
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Local Similarity 48.2%;
les 120; Conservative 3
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APPLICATION NUMBER: 60/049,019
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CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120
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                                                                                  LSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
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Pred. No. 3.5e-52;
15; Mismatches 89;
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US-09-025-059-1
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US-09-025-059-1
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                                                                                                                                               Query Match
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APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASCEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LIBRARY: LULL
TONE: 2723646
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CITY: Palo Alto
                                                                                                                                Local Similarity
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3174 Porter Dr.
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; APPLICANT: Darrow, Andrew
APPLICANT: Qi. Jenson
APPLICANT: Qi. Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                   Sequence 14, Application US/09386642 Patent No. 6420157
                                                                                                                                                                      GENERAL
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CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 288
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APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation
FILE REFERENCE: ORT-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic
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                                                                                                                                                                    INFORMATION:
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Pred. No. 1.5e
21; Mismatches
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ches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KLASS, MICHAEL R.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWEN D.
TITLE OF INVENTION: NOVEL SERIO
TITLE OF INVENTION: OF THE PROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
         NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/235-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic
                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
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APPLICANT:
APPLICANT:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park
                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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847/938-2623
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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Pred. No. 3.8e-50;
4; Mismatches 79
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RESULT 14
US-08-956-267A-2
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GENERAL INFORMATION:
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Best Local Similarity
Matches 119; Conser
                                                                                      APPLICATION NUMBER: US/08/956,267A
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4500.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 248 amino acids
                                                           TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 248 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 62324
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LIM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WOLDIKE, Helle Fabricius APPLICANT: KJELDSEN, Thomas Borglum TITLE OF INVENTION: A PROCess FOY PUTITLE OF INVENTION: (Trypsinogen)
                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
LENGTH: 24, TYPE; amino acid
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                            247 amino acids
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E: No. 6232456e
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47.8%; Pred. No. 3.9e-50;
htive 36; Mismatches 87;
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8166
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8166
LENGTH: 290
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Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 SWWYCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 SSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRIT 181
                                                                                                                                                                                                                                                                                                                                                                                           13 GLSQAATPKIFN------GTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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                                               ITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV 238
                                                                                                                                                                                                                                                                                                                                         GVSQESS-KVLNTNGTSGFLPGGYTCFPHSQPWQAALLVQGRLLCGGVLVHPKWVLTAAH
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ITDNMLCAGTKEGGKDSCEGDSGGPLVCNRTLYGIVSWGDF-PCGQPDRPGVYTRVSRYV
                                                                                                                                                                TSSVQPLPLP-NDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                        CLKEGLKVYLGKHALGRVEAGEQVREVVHSIPHPEYRRSPTHLNHDHDIMLLELQSPVQL 149
                                                                                                                                                                                                                                                                             CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST -- SHEHDLRLLRLRLPVRV 120
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                                                                                                       TGYIQTLPLSHNNRLTPGTTCRVSGWGTTTSPQVNYPKTLQCANIQLRSDEECRQVYPGK
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46.8%; Pred. No. 4.4e-47;
rative 36; Mismatches 80;
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OF DETECTION AND USES THEREOF
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ompleted: March : 46 secs	269 LWIRETIR 276	239 DWIRMIMR 246
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Maximum DB seg length: 200000000
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n on:
                                                                                                                                                                        AAY99393 standard; protein; 248 AA.
Human PRO1303 (UNO669) amino acid s
WO200012708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB21304 standard; protein; 248 AA.
Human KLK-L5 protein #4.
WO200053776-A2.
                                                                                                                                                                                                                 02000.
14-SEP-2000.
(GETH ) GENENTECH INC.
(GETH ) 100.0%;
                                                                                                                                                                                                                                                                                                                                                                           AAB24428 standard;
Human PRO1303 proto
WO200032221-A2.
                                                                         WO200154477-A2.
                                                                                                                                                                                                                                                                                    AAB24032 standard; protein; 248 AA.
Human PRO1303 protein sequence SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                08-JUN-2000
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 AAB66142 standard;
                                                (HYSE-) HYSEQ INC.
                                                                                    AAM23994 standard; protein;
Human EST encoded protein SI
                                                                                                                                                                09-MAR-2000
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14-SEP-2000.
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d. No. is the number of results predicted by chance to have re greater than or equal to the score of the result being pris derived by analysis of the total score distribution.
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Similarity 100.0%;
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                                                                                                                                                   GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
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2105692 seqs, 386760381 residues
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1374
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Listing first 1500
                                                                                                                                                                                                                                                                                                                                                                                       dard; protein; 248 AA.
protein sequence SEQ
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geneseqp2003as:*
geneseqp2003bs:*
protein; 248 AA
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SEQ ID NO:
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                        1374;
No. 5e
                                                                                                                          1374;
No. 56
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No. 5e-98;
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Best Local Similarity
RESULT 12
ID ADD39786 standard; pr
DE Human secreted/transm
PN US2003083462-A1.
PD 01-MAY-2003.
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Best Local S
RESULT 14
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RESULT 7
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RESULT 13
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ID ABO4
DE Huma
PN US20
 Best Local Similarity
RESULT 15
ID ADD39309 standard;
DE Human secreted/tran
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Best Local Similarity
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US2003064925-A1.
03-APR-2007
                                                                                                                                                                                                                                                                                                                                                      ADD70709 standard; protein; 2
Human secreted/transmembrane
US2003099625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO33512 standard; protein; 248 AA. Novel human secreted and transmembrane US20030731199-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane protein US2003044841-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO33635 standard; protein; 248 AA.
Novel human secreted and transmembrane
US2003073130-A1.
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                                                                   US2003096955-A1.
22-MAY-2003.
                                                                                          ADD38353 standard; protein; !
Human secreted/transmembrane
                                                                                                                                                                                ADD70232 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
                                                                                                                                                                                                                                                               Human secreted/transmembrane US2003083462-A1.
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ADD39309 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
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                                                                                                                                                                        US2003054406-A1.
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ADH99387 standard; protein; 248 AA Human secreted/transmembrane prote: US2003065142-A1.
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US2003069179-A1.
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ID ADE96567 standard; p.
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   ADH04513 standard; protein; 2
Human secreted/transmembrane
US2004005626-A1.
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16-OCT-2003 (GETH ) GENENTECH INC.
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Human secreted/transmembrane protein PRO1303.
US2003203401-A1.
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23-OCT-2003.
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Human KLK-L5 protein #3.
WO200053776-A2.
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Human kallikrein-like protein 5 (18817)
WQ2003039475-A2.
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US2004014130-A1.
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                                                                                                    Human kallikrein 12,
WO2004029285-A2.
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Human PRO1303 protein.
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Human kallikrein 12,
WO2004029285-A2.
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Human secreted/transmembrane protein PRO1303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH )
                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                              (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                  L5-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-APR-2004
                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                              ocal Similarity
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2004.

) GENENTECH INC.

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100.0%;
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) GENENTECH INC.
100.0%;
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h 100.0%;
Similarity 100.0%;
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                            ; protein; 254
sequence SEQ
                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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, marker of e
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                                                           Score Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
endocrine
                            4 AA.
ID NO:2150
                                                                                                              endocrine
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                                                                                                                                             1301;
l. No. 2.
                                                            1301; DB 8;
. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                  1367;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1374; DB :
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No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1374; DB
No. 5e-98;
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No. 5e-98;
                                                                                                                                                                                                                                                                                                                 1.7e-97;
                                                                                                              cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
                                                                                                                                              DB 5;
.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                              8;
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Que.
Best L.
RESULT 47
ID AAY0'
DE Am'
PN V
PD
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RESULT 49
ID AAB44300 standard; p
DE Human PRO322 (UNQ283
PN W0200053756-A2.
PD 14-SEP-2000.
       Best 1
RESULT 1
ID AAI
DE Hui
PN WO:
PD 07
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ID 1
DE 1
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RESULT 46
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RESULT 44
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RESULT 43
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted w09940183-A1. 12-AUG-1999.
                                                                                               Human neuropsin protein. JP11318461-A. 24-NOV-1999.
                                                                                                                                                                                       AAB44300 standard; protein; Human PRO322 (UNQ283) prote: WO200053756-A2.
                                                                                                                                                                                                                                                                                                                                                    AAY03220 standard; protein; Amino acid sequence of humar W09909138-Al.
                                                                                                                                                                                                                                                                                                                                                                                                             WO9946281-A2.
16-SEP-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human serine JP11225765-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human KLK-L5 protein WO200053776-A2.
                                                       (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK
xy Match 45.9%; Score 630.0
t Local Similarity 50.2%; Pred. No. 1
                                                                                                                                                                    14-SEP-2000
(GETH ) GENI
                                                                                                                                                                                                                                                  (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                       WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO322 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY32852 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28642 standard; protein;
Human secreted protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB21301 standard;
                 WO200140466-A2.
                             Human
                                                                                                                             AAY51131 standard; protein;
                                                                                                                                                                                                                                                                                          AAB21322 standard;
                                                                                                                                                                                                                                                                                                                                           25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY41744 standard; protein;
                                     AAU12369 standard;
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                                                                                                                                                                   GENENTECH INC
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                                                                                      SHIOZAKA S.
                                                                                                                                                 Similarity
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GENENTECH INC
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                          polypeptide
                                                                                                                                                                                                                              15.9%;
50.2%;
                                                                                                                                                                                                                                                                                          protein;
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                                     protein;
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64.1%;
                                                                                                                                                45.9%;
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50.2%;
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                                     260 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AA.
cDNA clone HKAFV61.
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Pred.
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Pred.
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Pred.
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Pred. No. 2.
                                                                                                                                                                                                 sequence
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No. 8
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. No. 8.
                                                                                                                                                 630.
No.
                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                630.5; DB 3;
No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                             630.5; DB 2;
No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                               antigen
                                                        1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e-40;
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                                                                                                                                                                                                                                                                                                               .5; DB 2;
1.1e-40;
                                                                                                                                                                                                 SEQ
                                                                                                                                                 .5; DB 3;
1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
.5e-71;
                                                                     DB
                                                                                                                                                                                                  ID NO:395
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                                                                                                                                                                                                                                                                                                                                                              gene-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162;
                                                                                                                                                            260;
                                                                                                                                                                                                                                                                                                                                                               protein.
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RESULT 56
ID ABB95:
DE Human
PN WO2000
PD 31-JA.
PA (GETH
PA (GETH
PA (GERB
PA (GERB
PA (GODC
PA (GUDC
                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                    Query Match
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Best Local
                                                                        Novel human secreted US2003032156-A1.
                                                                                                                                                                                                                      ADI17076 standard;
Human NOVX protein
WO200268649-A2.
                                                                                                               ABO17813 standard;
                                                             L3-FEB-2003
                                                                                                                                                                                         (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human angiogenesis
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO322.
WO200109327-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiogenesis-associated prote W0200053753-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB95458 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001.
(GETH ) GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB84852 standard; protein;
Human PRO322 protein sequenc
WO200200690-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU81959 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG23373 standard; protein; 260 AA.
Novel human diagnostic protein #23364.
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB53087 standard;
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                      CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENENTECH INC.
BAKER K P.
FERRARA N.
                                        GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                   MOOD M
                                                                                                                                                                                                                                                                                                                                                                                                          PAN J.
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GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GODDARD A.
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                                                                                                                                                                                                                                       protein; 2
homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC.
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45.9%;
Y 50.2%;
                                                                                                             protein; 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
related p
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   50.
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                                                                                        and transmembrane
                                                                                                                                                                                                                                                                                           45.9%;
50.2%;
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sequence SEQ I
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50.2%;
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                                                                                                                                                 . 2%;
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                                                                                                                                                                                                                                       260 AA.
e SeqID
   Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 1.1e-40;
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Pred.
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630.5; DB 6;
No. 1.1e-40;
                                                                                                                                               630.5;
No. 1.
                                                                                                                                                                                                                                         612
                                                                                                                                                                                                                                                                                           630.5; DB 5;
No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO322
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No. 1.1e-40;
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No. 1.1e-40;
                                                                                                                                               .5; DB 5;
1.1e-40;
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Best Local Similarity
RESULT 62
ID ADAS702 standard; pr
DE Human NOV11h protein
PN W02003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
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Best Local Similarity
RESULT 67
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ID ABU72
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Novel secreted and t
US2003017563-A1.
23-JAN-2003.
(GETH ) GENENTECH IN
                                     Human secreted/transmembrane US2003036179-A1.
                                                                                                                           ABU61130 standard; protein;
Human PRO322 polypeptide.
US2002169284-A1.
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(GETH ) GENI
                                                                    ABO25038 standard;
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20-FER-200
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Local
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Novel human secret
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13-MAR-2003.
(GETH) GENENTECH INC.
45.9%; (
13-rity 50.2%;
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US2003073212-A1.
17-APR-2003.
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Human PRO polypoptide #198.
US2003082704-A1.
01-MAY-2003.
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                                                   ADA86424 standard; protein; 260 AA. Novel human secreted and transmembrane US2003082711-A1.
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US2003049816-A1.
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ADB15988
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Novel human secreted and transmembrane
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Best Local Similarity
RESULT 80
ID ADB30576 standard; pr
DE Human PRO polypeptide
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC
RESULT 86
ID ADA91
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RESULT 81
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(GETH ) GENENTECH INC.

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US2003087349-A1.
08-MAY-2007
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US2003087350-A1.
08-MAY-2003.
ADA91821 standard; protein; 260 AA. Novel human secreted and transmembrane
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #198.
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protein PRO322

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PN DE
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                                               Query Match
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                                                                                                                                                                                US2003000
01-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%; /
ADA12595 standard; protein; ; Human secreted/transmembrane US2003055216-A1.
                                                                       ABO19701 standard; protein; 260 AA. Novel human secreted and transmembrane US2003050240-A1.
                                                                                                                                                                                                                                                                                          Novel human secreted and transmembrane US2003082691-A1.
                                                                                                                                                                                                                      Human PRO polypeptide #198.
US2003082710-A1.
01-MAY-2003
                                                                                                                                           Novel human secr
US2003044945-A1.
06-MAR-2003.
                                                          (GETH )
                                                                   13-MAR-2003
                                                                                                                                    (GETH )
                                                                                                                                                                      ABO43346 standard;
                                                                                                                                                                                                                                                                                                                                                                              ADA94060 standard; protein;
Human PRO polypeptide #198.
US2003077722-A1.
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                                                                                                                                                                                                                                                                                                                                                                       24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB14884 standard; protein;
Human PRO polypeptide #198.
US2003087351-A1.
                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted US2003073211-A1.
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01-MAY-2003.
(GETH ) GENENTEC
                                     Local Similarity
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                                                                                                                                                          346 standard; protein; 260 AA. human secreted and transmembrane
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2003.
) GENENTECH INC.
45.9%;
50.2%;
                                                      GENENTECH INC.
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ed and transmembrane
                                    45.9%;
50.2%;
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50.2%;
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Pred. No. 1.1e-40;
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Pred.
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Pred.
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                                    630.5; DB 6;
No. 1.1e-40;
                                                                                                             630.5; DB 6;
No. 1.1e-40;
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No.
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No. 1.1
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No. 1.1e-40;
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1.1e-40;
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Best Local Similarity
RESULT 102
ID ADB30024 standard; p
DE Human PRO polypeptid
PN US2003073214-A1.
PD 17-APR-2003.
     Best
RESULT
ID AD
DE Hu
PN US
PD 01
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RESULT 98
ID ADA82279 standard; p
DE Human PRO polypeptid
PN US2003082701-A1.
PD 01-MAY-2003.
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RESULT 101
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Best Local Similarity
RESULT 103
ID ADA80552 standard;
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ID ADA75
DE Human
PN US200
PD 17-AP
PA (GETH
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Best Local Similarity
RESULT 100
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RESULT 97
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Human PRO polypeptide #198. US2003082703-A1.
                                                                        Human PRO polypeptide #198. US2003082761-A1. 01-MAY-2003.
                                                                                                                                                                      AUB30024 standard; protein;
Human PRO polypeptide #198.
                                                                                                                                                                                                                  US2003082708-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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US2003082695-A1.
                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                          ADA84768 standard;
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                                                                                                                                                                                                                                                                                                                                     ADA85320 standard;
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Human PRO polypeptide #198.
US2003073216-A1.
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(GETH ) GENI
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US2003077713-A1.
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Human PRO polypeptide SEQ ID
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(GETH ) GENI
                                                 Local Similarity
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                                                                                                                                                                                                                                               768 standard; protein; 260 AA. human secreted and transmembrane
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2003.
) GENENTECH INC.
45.9%; 5
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JO-Al.

JO-Al.

2003.

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JOHN | GENENTECH 1

Best Local Similarity

RESULT 113

ID ADAB1104 stands

DE Human PRO 5

PN US20035

PD 01.
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RESULT 107
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              Human PRO polypeptide #198. US2003082702-A1.
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US2003077721-A1.
24-APR-2007
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US2003073210-A1.
17-APR-2007
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Human PRO polypeptide SEQ II
US2003077715-A1.
24-APR-2003.
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13-MAR-2003.
(GETH) GENENTECH
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Human PRO polypeptide #198.
US2003092147-A1.
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Best Local Similarity RESULT 122
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RESULT 120
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01-MAY-2003.
(GETH ) GENENTECH INC.
45.9%; (
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01-MAY-2003.
(GETH) GENENTECH INC.
(GETH) 45.9%; /
March 17-ity 50.2%;
                                                                                                        Novel human secreted and transmembrane US2003082700-A1.
                                                                                                                                                                                                 Novel human secreted and transmembrane US2003082709-A1.
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                                       ADA46467 standard; protein; Novel human secreted and traus2003054516-A1.
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US2003049633-A1.
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Human PRO polypeptide #198.
US2003077710-A1.
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01-MAY-2003.
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polypeptide #198.
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US2003022239-A1.
30-JAN-2003
ADB23651 standard; protein;
Human PRO polypeptide SEQ I
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Human PRO polypeptide #198.
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US2003087344-A1.
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                                             (GETH ) GENENTECH INC.
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Human PRO polypeptide #198.
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(GETH) GENENTECH INC.
(GETH) 45.9%;
Match 45.9%;
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W02102102235-A2.

27-DEC-2002.
Novel human secreted and tra
US2003082764-Al.
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(GETH) GENENTECH INC.
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Human PRO polypeptide #198.
US2003082762-A1.
01-MAY-2003.
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Human PRO polypeptide #198.
US2003082698-A1.
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Novel human secreted and transmembrane
US2003082689-A1.
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US2003087347-A1.
08-MAY-2003
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US2003082766-A1.
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   Human PRO polypeptide SEQ ID NO 396 US2003077718-A1.
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Human PRO polypeptide #60.
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No. 1.1
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No. 1.1e-40;
                                          630.5; DB 7
No. 1.1e-40;
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No. 1.1e-40;
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1.1e-40;
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Best Loca
RESULT 153
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Best Local Similarity
RESULT 158
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Best Local Similarity
RESULT 156
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RESULT 155
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                                                                                         ADC63051 standard; protein; 
Human secreted/transmembrane
US2003068648-A1.
                                                                                                                                                            ADC68991 standard; protein; a Human secreted/transmembrane US2003064407-A1.
                                                                                                                                                                                                                                                                                                                              ADC63767 standard; protein; 
Human secreted/transmembrane
US2003054405-A1.
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                                                                                                                                                                                                                                         US2003060406-A1.
27-MAR-2003.
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Human secreted/transmembrane
US2003049684-A1.
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            Human secreted/transmembrane US2003069178-A1.
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No. 1.1e-40;
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GENENTECH INC.

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RESULT 167
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RESULT 160
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Best Local (
                         Novel human secreted and transmembrane US2003087366-A1.
                                                                                                       Novel human secreted and transmembrane US2003087365-A1.
                                                                                                     08-MAY-2003
                                                                                                                                                                                          ADC59963 standard; protein; 260 AA. Novel human secreted and transmembrane US2003092105-A1.
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Novel human secreted and tra
US2003092107-A1.
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                                                                                             (GETH )
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Human secreted/transmembrane
US2003104998-A1.
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Best Local Similarity
RESULT 169
ID ADC60515 standard; p
DE Novel human secreted
PN US2003087367-A1.
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Best Local Similarity
RESULT 176
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RESULT 175
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US2003092104-A1.
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(GETH ) GENENTECH INC.

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Match 45.9%; (
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08-MAY-2003.
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                                                                                                                                                                                                           08-MAY-2003
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US20030873672-71
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US2003087362-A1.
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Novel human secreted and tra
US2003087361-A1.
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(GETH ) GENENTECH INC.
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Pred. No. 1.1e-40;
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630.5; DB 7;
No. 1.1e-40;
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                                                                                   630.5; DB 7;
No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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RESULT 178

ID ADC90213 standard; protein; 260 AA.

DE Novel human secreted and transmembrane
PN US2003087348-A1.
PD 08-MAY-2003.
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Best Local Similarity
RESULT 183
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16-OCT-2003.
(GETH ) GENENTECH INC.
45.9%; (
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Human PRO polypeptide #198.
US200319473-A1.
16-OCT-2002
                             ADD10361 standard; protein; 2
Human secreted/transmembrane
US2003105011-A1.
05-JUN-2003.
                                                                                                                   ADD11088 standard; protein;
Human PRO polypeptide #198.
US2003194774-A1.
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Human kallikrein 8
WO2003085404-A1.
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ry Match 45.9%;
Local Similarity 50.2%;
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Novel human secreted and transmembrane
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08-MAY-2003.
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Human PRO polypeptide #198.
US2003194776-A1.
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) GENENTECH INC.
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RESULT 191
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RESULT 196
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RESULT 195
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US2003203437-A1.
30-CCT-2003.
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US2003087358-A1.
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US2003203438-A1.
                                                     ADD37114 standard; protein; i
Human secreted/transmembrane
US2003105012-A1.
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Human PRO polypeptide #198.
US2003104700
ABW00074 standard; protein;
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Best Local Similarity
RESULT 203
ID ADD91426 standard; p
DE Human PRO polypeptid
PN US2003199055-A1.
PD 23-OCT-2003.
    BE
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RESULT 200
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Best Local Similarity
RESULT 202
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RESULT 198
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Human PRO polypeptide #198.
US2003194779-A1.
16-OCT-2003.
(GETH) GENENTECH INC.
                                                                  ADE04040 standard; protein;
Human PRO polypeptide #198.
US2003199057-A1.
                                                                                                                                             Human PRO polypeptide #198. US2003199055-Al.
   Novel
           ADE32337 standard;
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Human PRO polypeptide #198.
US2003199030-A1.
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30-OCT-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%; /
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Human secreted/transmembrane
US2003096744-A1.
                                                                                                                              (GETH ) GENENTECH INC
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Novel human secreted and tra
US2003203432-A1.
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US2003203431-A1.
30-OCT-2003
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Human PRO polypeptide #198.
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30-OCT-2003.
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and transmembrane
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in; 260 AA.
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No. 1.1e-40;
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Best Local Similarity
RESULT 213
ID ADD91978 standard; p
DE Human PRO polypeptid
PN US2003199053-A1.
                              Query Match
Best Local S
RESULT 214
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Best Local Similarity
RESULT 207
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RESULT 206
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ADE33441 standard; protein, Novel human secreted and tra US2003194767-A1.
                                                                 Human PRO polypeptide #198. US2003199053-A1. 23-OCT-2003.
                                                                                                                                                    ADE17846 standard; protein;
Human PRO polypeptide #198.
US2003199023-A1.
23-OCT-2003.
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                                                             (GETH )
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                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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Human secreted/transmembrane
US2003203434-A1.
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Human PRO polypeptide #198.
US2001201479 אין
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16-OCT-2003.
(GETH ) GENENTEC
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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protein PRO322.

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Best Local Similarity
RESULT 223
ID ADE22821 standard; F
DE Human PRO polypeptic
PN US2003199064-A1.
PD 23-OCT-2003.
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RESULT 221
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16-OCT-2003.
(GETH) GENENTECH INC.
45.9%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%; (
45.9%; (
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US2003199059-A1.
23-CCT-2007
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US2003199026-A1.
23-OCT-200
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US2003199025-Al.
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US2003194768-A1.
16-OCT-2007
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Human secreted/transmembrane
US2003194781-A1.
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US2003194791-A1.
16-CCT-2003.
         Human PRO polypeptide #198
US2003199064-A1.
                                                                                                                                                           ADE43146 standard; protein;
Human PRO polypeptide #198.
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Human PRO polypeptide #198.
US2003207417-A1.
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Best
RESULT
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Best Local Similarity
RESULT 231
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Best Local Similarity
RESULT 230
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US2003207418-A1.
06.NOV-2003.
Human PRO polypeptide #198. US2003194777-A1. 16-OCT-2003.
                                                                           Human PRO polypeptide #198. US2003199034-A1.
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Human PRO polypeptide #198.
US2003199028-A1.
23-OCT-2003.
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Novel human secreted and tra
US2003194766-A1.
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Human PRO polypeptide #198.
US2003203429-A1.
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Human PRO polypeptide #198.
US2003199032-A1.
23-OCT-2003.
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RESULT
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PD 06
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Best Local Similarity
RESULT 240
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RESULT 238
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RESULT 235
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Best Local Similarity
RESULT 236
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Best Local Similarity
RESULT 233
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                     Novel human secreted and transmembrane US2003207381-A1. 66-NOV-2003.
                                                                                                          Human PRO polypeptide #198. US2003207372-A1. 06-NOV-2002
                                                                                                                                                                                             Human secreted/transmembrane US2003206915-A1.
                                                                                                                                                                                                                ADG60312 standard;
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Human secreted/transmembrane
US2003215651-A1.
20-NOV-2003.
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US2003207370-Al.
06-NOV-2003
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                                                                                                                                                                        (GETH ) GENENTECH INC.
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06-NOV-2003.
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Novel human secreted and transmembrane protein PRO322
US2003207355-A1.
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RESULT 247
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SULT 242
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Novel human secreted
US2003087353-A1
08-MAY-2003.
                                   Cancer/angiogenesis/fibrosis-related W02003042661-A2.
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08-MAY-2003.
                                                                                                                                            Novel human secreted and
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Novel human secreted and transmembrane
US2003207379-A1.
06-NOV-2003.
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US2003211571-A1.
13-NOV-2003.
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Human PRO polypeptide #198.
US2003100087-A1.
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US2003087357-Al.
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Human PRO polypeptide #198.
US2003092113-A1.
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15-MAY-2003.
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Novel human secreted and tra
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RESULT 267
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                                              Human PRO polypeptide #198. US2003199054-A1.
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                                                                                                                               ADE18398 standard; protein;
Human PRO polypeptide #198.
US2003194794-A1.
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Human PRO polypeptide #198.
US2003199062-A1.
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US2003092108-A1.
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RESULT 271
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RESULT 270
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                                 ADE91138 standard; protein;
Human PRO polypeptide #198.
US2003199061-A1.
23-OCT-2003.
                                                                                                       Human PRO polypeptide #198.
US2003199027-Al.
23-OCT-2000
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Human secreted/transmembrane protein,
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GODOWSKI P J.
GIRMALDI J C.
GURNEY A L.
HILLAN K J.
KLJAVIN I J.
KUO S S.
NAPIER M A.
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BOTSTEIN D.
DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
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STEWART T A.
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Best Local Similarity
RESULT 283
ID ADF27816 standard; p
DE Human secreted/trans
PN US2003199437-A1.
PD 23-OCT-2003.
  RESULT 284
ID ADE922
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Best Local Similarity
RESULT 282
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RESULT 276
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23-OCT-2003.
(GETH) GENENTECH INC.
(GETH) 45.9%;
Match 45.9%;
50.2%;
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Human secreted/transmembrane
US2003194780-A1.
16-OCT-2003.
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Human PRO polypeptide #198.
US2003199060-A1.
23-OCT-2003.
                    Local
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standard; protein;
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Human secreted/transmembrane
US2003194410-A1.
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Human secreted/transmembrane protei
US2003211092-A1.
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Human PRO polypeptide #198.
US2003199063-A1.
23-OCT-2003.
                                                                                         ADE91733 standard; protein; 260 AA.
Novel human secreted and transmembrane
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Human secreted/transmembrane protein,
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ADG02312 standard; protein;
Human PRO polypeptide #198.
                                                                               US2003199058-A1.
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Pred. No. 1.1e-40;
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No.
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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Best Local Similarity
RESULT 294
ID ADG22098 standard; p
DE Novel human secreted
PN US2003207360-A1.
PD 06-NOV-2003.
                              Best
RESULT
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US2003208055-A1.
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US2003207353-A1.
         ADG05241 standard; protein;
Human PRO polypeptide #198.
                                                                                   ADG16782 standard; protein;
Human PRO polypeptide #198.
US2003207359-A1.
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Human PRO polypeptide #198.
US2003207376-A1.
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US2003207375-A1.
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RESULT 311
ID ADG24929 standard; p
DE Novel human secreted
PN US2003207427-A1.
PD 06-NOV-2003.
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RESULT 309
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Novel human secreted and tra
US2003207427-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.9%;
- Match 45.9%;
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Human PRO polypeptide #198.
US2003207374-A1.
                                                                (GETH ) GENENTECH
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Human PRO polypeptide #198.
US2003207371-A1.
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Human PRO polypeptide #198.
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US2003207424-A1.
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27-NOV-2003.
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US2003207357-A1.
06-NOV-2003
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Human PRO polypeptide #198.
US2003207425-A1.
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(GETH ) GEN
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RESULT 320

ID ADG55825 standard; p
DE Novel human secreted
PN US2003207365-A1.
PD 06-NOV-2003.
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RESULT 319
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RESULT 318
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RESULT 317
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RESULT 313
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06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane
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US2003207358-A1.
06-NOV-2003
                                                                                    (GETH ) GENENTECH INC.
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Novel human secreted and transmembrane
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US2003207390-A1.
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US2003207356-A1.
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US2003207150-1
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                            Novel human secreted and transmembrane US2003207419-A1.
                                                                                                   Human PRO polypeptide #198. US2003077723-A1.
                                                                                                                                                                                                                                              ADG50568 standard; protein; i Human secreted/transmembrane US2003207803-A1.
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Novel human secret
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US2003207416-A1.
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                                                       ADG48696 standard; protein; Human secreted/transmembrane
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Novel human secreted and transmembrane
US2003207366-A1.
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Human PRO polypeptide #198.
US2003194793-A1.
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Human secreted/transmembrane
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Novel human secreted and transmembrane
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Best Local Similarity
RESULT 355
ID ADI37154 standard; p:
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RESULT 357
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RESULT 353
ID ADI14731 standard; p.
DE Novel human secreted
PN US2003207383-A1.
PD 06-NOV-2003.
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RESULT 349
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04-FEB-2004.
(GETH) GENENTECH INC.
(GETH) 45.9%;
Match 45.9%;
50.2%;
 Human
                                                                                      ADJ63607 standard; protein; 260 AA. Novel human secreted and transmembrane
          ADJ77502 standard;
                                                                    26-FEB-2004
                                                                            Novel human secr
US2004039164-A1.
                                                                                                                                                                                            ADI37154 standard; protein;
                                                                                                                                                                                                                                                                                                                                                      ADI14731 standard; protein; 260 AA. Novel human secreted and transmembrane US2003207383-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG09276 standard; protein; 260 AA. Novel human secreted and transmembrane US2004009547-A1.
                                                         (GETH )
                                                                                                                                                                        Human TADG-14 protein.
US2003199010-A1.
                                                                                                                                                                                                                                           06-NOV-2003
(GETH ) GEN
                                                                                                                                                                                                                                                                           ADI18326 standard; protein; 260 AA. Novel human secreted and transmembr
                                                                                                                                                                                                                                                                US2003207349-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI15399 standard; protein; 260 AA. Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG09928 standard; protein; 260 AA. Novel human secreted and transmembrane US2004009548-A1.
                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                  Local Similarity
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50.2%;
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                                                      GENENTECH
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standard; protein;
polypeptide #198.
                               I INC.
45.9%;
y 50.2%;
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45.9%;
cy 50.2%;
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homologue
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50.2%;
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No. 1.1e-40;
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No. 1.1e-40;
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(GETH )
Query Match
Best Local &
RESULT 358
ID ADK828'
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PN US2'
PD 0'
PA O'
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RESULT 363
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RESULT 361
ID ADM17394
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RESULT
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RESULT 359
   Best Local Similarity
RESULT 362
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26-FEB-2004
(GETH ) GENENTEC
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US2004058424-Al.
25-MAR-2004
                                                                                                                                                                                                                                                                                                  ADL07228 standard; protein; 7
Human secreted/transmembrane
US2004063921-A1.
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US2004048332-A1.
11-MAR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM27760 standard; protein;
Human PRO polypeptide #198.
US2004048333-A1.
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Human PRO polypeptide #198.
US2004038335-A1.
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Human PRO polypeptide #36.
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US2004038223-A1.
26-FEB-2004.
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(GETH ) GENENTECH INC.
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                                                                                             (XEXO/
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MILLET I.
PEYMAN J A.
KEKUDA R.
JU J.
LI L.
GUO X.
SPYTEK K A.
SPYTEK K A.
EDLIGER S R.
ELLERMAN K.
MALYANKAR U M.
ORT T.
GORMAN L.
ZERHUSEN B D.
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Pred. No. 1.1
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No. 1.1e-40;
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No. 1.1e-40;
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Query Match
Best Local Similarity
RESULT 371
ID AAB37985 standard; p
DE Human secreted prote
PN WO200055371-A1.
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Best Local Similarity
RESULT 368
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Best Local Similarity
RESULT 367
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Human PRO polypeptide #198.
US2004077064-A1.
22-APR-2004.
                                                                                                                                                                                                                                                                                                               ADI95828 standard; protein;
Human PRO polypeptide #198.
US2003077659-A1.
                                                                                                                                               WO2004075713-A2.
10-SEP-2004.
        AAB37985 standard; protein;
Human secreted protein encod
                                                          (SUNR ) SUNTORY LTD.
                                                                   24-AUG-1999.
                                                                            JP11225765-A.
                                                                                    AAY32853 standard; protein; 305 AA.
Human serine protease protein sequence.
                                                                                                                 (MOUN ) MOUNT SINAI HOSPITAL.

ry Match 45.9%;
t Local Similarity 50.2%;
                                                                                                                                                                  Human ovarian
                                                                                                                                                                            ADR72883 standard;
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US2003207354-A1.
                                                                                                                                                                                                                                                      ADI96380 standard; protein;
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2004.
) GENENTECH INC.
45.9%; ...
3.1.V 50.2%;
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) RIEGER D K.
) SPADERNA S K.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
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BERGHS C.
DIPIPPO V A.
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RASTELLI L.
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50.9%;
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tumour marker kallikrein
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No. 1.1e-40;
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No. 1.1e-40;
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No. 1.1e-40;
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                                      DB 2;
           clone
           HWJAE49
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                                                305;
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Query Match
Best Local Similarity
RESULT 378

ID ABB57219 standard; p
DE Mouse ischaemic cond
PN W0200188188-A2.
PD 22-NOV-2001.
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Best Local S
RESULT 379
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DE
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RESULT 374
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Best Local Similarity
RESULT 372
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Mouse neuropsin
US6642013-B1.
                                                                                    ADI17073 standard; I
Murine NOVX protein
WO200268649-A2.
                     ADI39731 standard;
                                                                                                                           (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

TY Match
45.3%; Score 622.5; DB 5

Local Similarity 49.0%; Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                        Human protease HUPM-7.
WO9936550-A2.
22-HTT.-1000
                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1996.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO
21TY MATCh
45.3%; Score 62
21TY MATCH 49.0%; Pred. NC
                                                                                                                                                                                                                                       22-JUL-1999.
(INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                 Mouse neuropsin protein. JP08311099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A human serine protease designated EP887414-A2.
                                                                                                                                                                                                                                                                                                                                                                     AAW12393 standard; protein; 260 AA
                                                                CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                      JP08245700-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB21311 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP41332 standard; pro
Human ovarian antigen
WO200200677-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000
                                                                                                                                                                                                                                                                                                                             SHIO/) SHIOZAKA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW10694 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK) SMITHKLINE BEECHAM PLC.

ry Match
Local Similarity 50.4%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOUN ) MOUNT SINAI
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                                          Local Similarity
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                                                                                                                                                                                                                                                                                                       ocal Similarity
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           protein.
                                                                                                                                                                                   rd; protein; condition re
                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropsin,
                    protein;
                                                                                                         protein;
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gen HCOQP78, s
                                                                                             homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOSPITAL.
45.6%; ;
50.4%; ;
                                          45.3%;
                                                                                                                                                                                                                  45.3%;
                                                                                                                                                                                                                                         INC
                                                                                                                                                                                                                                                                                                        45.3%;
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45.6%; ;
50.9%; ;
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45.6%;
50.9%;
                                                                                                                                                                                 n; 260 AA.
related protein
                     260
                                         Score
Pred.
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, used for
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Pred.
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Pred.
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                                                                                             SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 626.5; DB 3; Pred. No. 2.3e-40;
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Pred.
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Pred.
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                                         622.
No.
                                                                                                                                                                                                                  622.5; DB 2;
No. 4.5e-40;
                                                                                                                                                                                                                                                                                                       622.5; DB 2;
No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                          622.5; DB 2;
No. 4.5e-40;
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No. 2.
                                                                                             609
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No. 2.2e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627; DB 3;
No. 2.4e-40;
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                                        4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody
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.4e-40;
                                                                                                                                                                                  sequence
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A (HUMA-)

Query Match
Best Local S'
RESULT 388
ID AAU83f
DE Huma
PN WO'
PD
  RESULT
ID AB
DE Pr
PN WC
PD 18
PD 18
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RESULT 384
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RESULT 381
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                                                        Query Match
Best Local :
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                                                                                                                                              Human secreted protein encoded be WO200162891-A2.
30-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ry Match
                  ABG61816 standard; protein; Prostate cancer-associated; WO200230268-A2.
                                                                                             Human PRO protein, WO200208288-A2.
18-APR-2002.
(EOSB-) EOS
                                                                                                                AAU83684 standard;
                                                                                                                                                                                                                                  07-JUN-2001
(GETH ) GEN
                                                                                                                                                                                                                                                  AAU12424 standard; protein; 250 AA
Human PRO1279 polypeptide sequence
WO200140466-A2.
                                                                                                                                                                                                                                                                                                                             AAB66139 standard; protein; 2 Protein of the invention #51. W020078961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       AAY99390 standard; protein;
Human PRO1279 (UNQ649) amino
WC200012708-A2.
                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200268649-A2.
06-SEP-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOUN ) MOUNT SINAI HOSPITAL.
PRINT MATCH 45.0%;
The Local Similarity 48.2%;
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WO200053776-A2.
                                                                                                                                                                                                                                                                                                             (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB21325 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat NOVX protein
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US2003199010-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI17074 standard;
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                                                       Similarity
                                                                          GENENTECH INC.
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homologue
                                                                                                     protein; 250 AA.
Seq ID No 186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                  SCI INC.
45.0%;
48.2%;
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48.2%;
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48.2%;
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48.2%;
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48.2%;
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amino acid s
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                          ; 250 AA.
protein
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SeqID
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Pred.
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Pred. No. 8.7e-40;
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Pred. No.
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No. 8.7e-40;
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No. 8.7e-40;
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No.
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No.
                                                                                                                                  8.5; DB 4;
8.7e-40;
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8.7e-40;
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BIOTECHNOLOGY

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Best Local Similarity
RESULT 394
ID ARCORDO
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RESULT 392
ID ABO17868 standard; p
DE Novel human secreted
PN US2003032156-A1.
PD 13-FEB-2003.
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Best Local S
RESULT 395
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                                                                                                                                                                                                   Human PRO polypeptide #253.
US200304311-A1.
02-JAN-2003.
(GETH ) GENENTECH TWO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU80831 standard; protein;
Human PRO polypeptide #93.
US2003036635-A1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                ABO33797 standard; protein; 250 AA. Novel human secreted and transmembrane US2003045687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO17868 standard; protein; 250 AA.
                                                                               Lung cancer-associated WO200286443-A2.
                                                                                                ABU56739 standard, protein; 250 AA Lung cancer-associated polypeptide
                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB95526 standard; protein; 250 AA.
Human angiogenesis related protein PRO1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002.
(GETH ) GENENTECH
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(FERR/)
(GERB/)
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/ Match
Local Similarity
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOOD W I.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FERRARA N
GERBER H.
EOS BIOTECHNOLOGY INC.
h 45.0%; Score
Similarity 48.2%; Pred.
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  618.5; DB 6;
No. 8.7e-40;
                                                                                                    #332.
                                                                                                                                                              618.5; DB 6;
No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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Best Local Similarity RESULT 405
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RESULT 399
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                        Human PRO polypeptide #253.
US2003054517-A1.
20-MAR-2003.
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Human PRO polypeptide #253.
US2003036180-A1.
20-FEB-2003.
                                                                                                                   ABJ72320 standard; protein;
Human PRO1279 protein.
US2003050448-A1.
                                                                                                                                                                                                 ADA76456 standard; protein;
Human PRO polypeptide #253.
US2003073212-A1.
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Human secreted/transmembrane 
US2003036179-A1.
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Novel secreted and transmembrane
US2003017563-A1.
                                                                                                                                                                                                                                                                         Novel human secretus2003022328-A1. 30-JAN-2003.
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US2003088063-A1.
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No. 8.7e-40;
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Best Local Similarity
RESULT 413
ID AB033632 standard; p
DE Novel human secreted
PN US2003073130-A1.
PD 17-APR-2003.
                                                                                           Best Local Similarity RESULT 414
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RESULT 408
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                                              Human PRO polypeptide #253. US2003068795-A1. 10-APR-2003.
 ADB30686
                                                                                                                                         ABO33632 standard; protein; 250 AA.
Novel human secreted and transmembrane
US2003073130-A1.
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Human PRO polypeptide #253.
US2003087350-A1.
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Novel human secreted and transmembrane
US2003082711-A1.
(GETH) GENENTECH INC.
          Local Similarity
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Human PRO polypeptide #253.
US2003082704-A1.
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US2003049816-A1.
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Novel human secreted and transmembrane
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Best Local Similarity
RESULT 422
ID ADB14994 standard; p
DE Human PRO polypeptid
PN US2003087351-A1.
PD 08-MAY-2003.
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RESULT 420
ID ADB16839 standard; p
DE Human PRO polypeptid
PN US2003087349-A1.
PD 08-MAY-2003.
                     Best Local Similarity RESULT 424
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  ADA94170 standard;
Human PRO polypept
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Human PRO polypeptide #253.
US2003087351-A1.
                                                                             ADB18955 standard; protein; 250 AA.

Novel human secreted and transmembrane
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                                                                    US2003073211-A1.
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Human PRO polypeptide #253.
US2003087349-A1.
08-MAY-2003.
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Human PRO polypeptide #253.
US2003082705-A1.
01-MAY-2003.
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RESULT 428
ID ADA7466
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RESULT 431
ID ADA75352 standard; p:
DE Human PRO polypeptid
PN US2003073216-A1.
PD 17-APR-2003.
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US200307326-A1.
17-APR-2003
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01-MAY->>^>
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                                                                               ADA85430 standard; protein; 250 AA. Novel human secreted and transmembr US2003082695-A1.
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Human PRO polypeptide #253.
US2003068798-A1.
ADA84878 standard;
Novel human secretous2003082708-A1.
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Novel human secreted and transmembrane
US2003044945-A1.

06-MAR-2003.

(GETH ) GENENTECH INC.
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Human PRO polypeptide #253.
US2003082710-A1.
01-MAY-2003.
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Best Local Similarity
RESULT 442
ID ABJ72448 standard; p
DE Human PRO1279 protei
PN US2003027988-A1.
PD 06-FEB-2003.
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Best Local Similarity
RESULT 434
ID ADB30134 standard; p
DE Human PRO polypeptic
PN US2003073214-A1.
PD 17-APR-2003.
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Best Local Similarity
RESULT 451
ID ADA77663 standard; p
DE Human PRO polypeptid
PN US2003068797-A1.
PD 10-APR-2003.
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                                                                                       ABO34343 standard; protein; 
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US2003082760-A1.
01-MAY-2003
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US2003082765-A1.
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Novel human secreted and transmembrane
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Human PRO polypeptide #253.
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25-FER-200
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US2003073129-A1.
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                                                          ADB23761 standard; protein; ;
Human PRO polypeptide SEQ ID
US2003077712-A1.
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US2003087352-Al.
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                                                           ADB66718 standard; protein, Novel human secreted and tra US2003082689-A1.
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15-MAY-2003.
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                                                                                                                                                               ADB38246 standard; protein; 250 AA.

Novel human secreted and transmembrane protein
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US2003096968-A1.
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           ADB85053 standard;
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Similarity 48.
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standard; protein; polypeptide #93.
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No. 8.7e-40;
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No. 8.7e-40;
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WO2002102235-A2.
27-DEC-2002.
A (EOSB-) EOS BIOTECHNOLOGY INC.
45.0%; Score 61
Match 41-rity 48.2%; Pred. No.
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ADB83922 standard; protein; 250 AA. Novel human secreted and transmembrane US2003069397-A1.
                                                                          Novel human secreted and tra
US2003082687-Al.
01-MAY-2002
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Human PRO polypeptide #253.
US2003082698-Al.
01-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH 45.0%;
uery Match
45.0%;
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Human PRO polypeptide #93.
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US2003088067-A1.
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Human PRO polypeptide #93.
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Novel human secreted and transmembrane
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US2003082762-A1.
01-MAY-2003
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protein #81.
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Human PRO polypeptide SEQ ID US2003077720-A1.
                                                                              Human PRO polypeptide SEQ ID US200307718-A1.
                                                                24-APR-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                          ADB34071 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077716-A1.
                                                                                                                                                                                                                                                                                                    Human PRO polypeptide SEQ ID US200307717-A1.
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15-MAY-2003.
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US2003092106-Al.
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Human PRO polypeptide #93.
US2003096969-A1.
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Human PRO polypeptide #93.
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Human PRO polypeptide #51.
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US2003088064-A1.
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                               ADC49135 standard;
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618.5; DB 7;
No. 8.7e-40;
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                                                                                                                                                   No.
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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. 8.7e-40;
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8.7e-40;
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Query March
Best Local Similarity
RESULT 532
ID ADC77887 standard; p
DE Novel human secreted
PN US203088066-A1.
PD 08-MAY-2003.
                                                                        Best Local Similarity RESULT 533
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RESULT 531
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Best Local Similarity
RESULT 530
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                                                                                                                    Novel human secreted and transmembrane US2003088066-A1.
                                                                                                                                                                                                                                                                           Human secreted/transmembrane US2003105011-A1.
                                                 ADC80139 standard; protein; 250 AA.
NOvel human secreted and transmembrane
                                 US2003087358-A1.
                                                                                                                                                                                                ADC48079 standard; protein;
Human PRO polypeptide #253.
US2003194771-A1.
16-OCT-2003.
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                                                                                                    (GETH ) GENENTECH
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Novel human secreted and transmembrane protein PRO1279.
US2003096972-A1.
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secreted and transmembrane
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Pred. No. 8.7e-40;
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O polypeptide #104
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No. 8.7e-40;
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RESULT 535
ID ADD09'
ID Hump
PN US'
PD 1
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RESULT 540
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Best Local Similarity
RESULT 542
Best Local Similarity RESULT 543 ID ADD53752 standard;
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Best Local Similarity
RESULT 538
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                                                                                                                                            Human secreted/transmembrane US2003083462-A1.
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                                                           ADD53200 standard; protein;
Human PRO polypeptide #253.
US2003194792-A1.
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US2003105290-A1.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                ADD39762 standard; protein; 250 AA
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                                                                                                                                                                                                                                       Human secreted/transmembrane protein PRO1279.
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transmembrane
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Pred.
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                    618.5; DB 7
No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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RESULT 545
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RESULT 546
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                                                                    ADD02141 standard; protein;
Human PRO polypeptide #253.
US2003203430-A1.
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                                                                                                                                              US2003096971-ĀĪ.
22-MAY-2003.
                                                                                                                                                               ADD50577 standard; protein;
Human PRO polypeptide #93.
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Human secreted/transmembrane
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30-OCT-2003.
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ADD54323 standard; protein; 250 AA.
Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2003
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ADE20072 standard; protein; : Human secreted/transmembrane US2003092883-A1.
                                                                            ADE04150 standard; protein;
Human PRO polypeptide #253.
US2003199057-A1.
                                                                                                                                                 Human PRO polypeptide #253, US2003199055-A1. 23-OCT-2003.
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US2003199030-A1.
23-OCT-2003
                                                        (GETH ) GENENTECH INC.
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US2003096970-A1.
22-MAY-2003
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Query Match
Best Local S:
RESULT 570
ID ADD80155 :
DE Human PRO
PN US2003207-
PD 06-NOV-200
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Best Local S
RESULT 568
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PN US2003194
PD 16-OCT-20
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16-OCT-2003.
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48.2%;
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US2003194791-A1.
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US2003199023-A1.
23-OCT-2007
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US2003199056-A1.
23-OCT-200
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Novel human secreted and tra
US2003194765-A1.
16-OCT-2003.
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Pred. No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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No. 8.7e-40;
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8.7e-40;
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Query Match
Best Local Similarity
RESULT 579
ID ADD79049 standard; pr
DE Human PRO polypeptide
PN US2003203429-A1.
PD 30-CCT-2003.
PA (GETH ) GENENTECH INC
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RESULT 576
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RESULT 577
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US2003199059-A1.
23-OCT------
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        Human PRO polypeptide #253.
US2003203429-A1.
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Human PRO polypeptide #253.
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Human PRO polypeptide #253.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #253.
US2003194768-A1.
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Human secreted/transmembrane protein PRO1279.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #253.
US2003199025-A1.
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Query Match
Best Local Similarity
RESULT 587
                                                Best Local Similarity RESULT 588
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16-OCT-2003.
(GETH ) GENENTECH INC.
45.0%;
Match 45.0%;
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                 ADF55859 standard; protein; Human secreted/transmembrane US2003204054-A1.
                                                                                       ADF29966 standard; protein; 
Human secreted/transmembrane
US2003204953-A1.
30-OCT-2003.
                                                                                                                                                                     ADE92947 standard; protein;
Human PRO polypeptide #253.
US2003194777-A1.
16-OCT-2003.
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Human PRO polypeptide #253.
US2003207418-A1.
06-NOV-2003.
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Human PRO polypeptide #253.
US2003199028-A1.
23-OCT-2003.
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US2003194766-A1.
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protein
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Best Loc
RESULT 591
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RESULT 597

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DE Novel human secreted
PN US2003207385-A1.
PD 06-NOV-2003.
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                                       Novel human secreted US2003207385-A1.
                                                                                                                    ADH99363 standard; protein; Human secreted/transmembrane US2003065142-A1.
                                                                                                                                                                                              Novel human secreted and transmembrane US2003207379-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.0%;
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Novel human secreted and transmembrane protein PRO1279.
US2003207381-A1.
                     (GETH ) GENENTECH INC.
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(GETH ) GEN
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US2003207372-A1.
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US2003207373-A1.
06-NOV-2003
                                                                                                  (GETH ) GENENTECH
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   Local Similarity
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08-MAY-2003.
(GETH ) GENENTEON ----
                                      ADN14981 standard; protein;
Novel human secreted and tra
US2003087357-A1.
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22-MAY-2003.
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08-MAY-2003.
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US2003100728-A1.
29-MAY-2003
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US2003100735-A1.
                                                          ADD85111 standard; protein; 250 AA. Novel human secreted and transmembrane US2003100722-A1.
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US2003092115-Al
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US2003203440-A1.
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Human PRO polypeptide #253.
US2003092113-A1.
15-MAY-2003.
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US2003100737-A1.
29-MAY-2003.
                                                                                ADD78483 standard; protein; 250 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #253.
US2003211571-A1.
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29-MAY-2003.
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Human secreted/transmembrane
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No. 8.7e-40;
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US2003100497-A1

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RESULT 632
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29-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.0%;
Match 17-rity 48.2%;
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29-MAY-2003 (GETH ) GENENTECH INC.
ADD85617 standard; protein; 250 AA Novel human secreted and transmemb; US2003100721-A1.
                                                                        US2003100718-A1.
29-MAY-2003.
                                                                                          ADD76125 standard; protein; 250 AA.
Novel human secreted and transmembrane
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US2003100708-A1.
29-MAY-2007
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15-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.0%;
MATCH 48.2%;
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US2003100709-A1.
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                                                              (GETH ) GENENTECH INC.
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Human PRO polypeptide #93.
US2003100064-A1.
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29-MAY-2003.
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(GETH ) GENENTECH
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Human PRO polypeptide #253.
US2003092108-A1.
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Best Local Similarity
RESULT 641
ID ADD86691 standard; p
DE Novel human secreted
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH IN
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RESULT 642
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RESULT 643
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29-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.0%;
Match 45.0%;
ADD78159 standard; protein;
Novel human secreted and tra
US2003100731-A1.
29-MAY-2003.
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US2003100715-A1.
29-MAY-2003
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15-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 45.0%;
Match 45.0%;
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Human PRO polypeptide #253.
US2003199062-A1.
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(GETH ) GEN
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Human PRO polypeptide #93.
US2003100726-A1.
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US2003203439-A1.
30-CCT-2000
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US2003092110-A1.
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Human PRO polypeptide
US2003092111-A1.
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RESULT 650
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US2003100713-A1.
29-MAY-2007
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US2003100710-A1.
29-MAY-2007
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US2003100730-Al.
29-MAY-2007
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Human PRO polypeptide #253.
US2003199054-A1.
         US2003100720-A1.
29-MAY-2003.
                                ADD85863 standard; protein; 250 AA. Novel human secreted and transmembrane
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Human PRO polypeptide #253.
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(GETH ) GEN
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RESULT 660
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US2003199052-A1.
23-OCT-2003.
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                            ADF24753 standard; protein; ;
Human secreted/transmembrane
US2003198993-A1.
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Human secreted/transmembrane
US2003199675-A1.
23-OCT-2003.
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Human PRO polypeptide #253.
US2003199061-A1.
23-OCT-2003.
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Human secreted/transmembrane
US2003195347-A1.
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Human PRO polypeptide #253.
US2003199027-A1.
23-OCT-2003.
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Human PRO polypeptide #93.
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Best Local Similarity
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Human PRO polypeptide #253.
US200319963-Al.
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Novel human secreted and transmembrane
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Human PRO polypeptide #253.
US2003199029-A1.
23-OCT-2003.
(GETH) GENENTECH INC.
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Human secreted/transmembrane
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Best Local Similarity
RESULT 677
ID ADF99307 standard; p.
DE Human PRO polypeptide
PN US2003207353-A1.
PD 06-NOV-2003
PA (GETH ) GENENTECH INC
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ID ADG22208 standard;
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US2003207353-A1.
06-NOV-2003.
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US2003207359-A1.
06-NOV-2007
                                                  Human PRO polypeptide #253.
US200120177775
                                    US2003207375-A1.
                                                                 ADG05351 standard;
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Human PRO polypeptide #253.
US2003207351-A1.
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Novel human secreted and transmembrane
US2003207426-A1.
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US2003207376-A1.
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No. 8.7e-40;
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RESULT 687
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RESULT 686
ID ADF97080 standard;
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ESULT 685
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US2003207425-A1.
06-NOV-2003.
                                                           ADG23849 standard; protein; 250 AA.
Novel human secreted and transmembrane
US2003207389-A1.
                                                                                                                                            ADG06265 standard; protein;
Human PRO polypeptide #253.
US2003207374-A1.
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Human PRO polypeptide #253.
US2003207371-A1.
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US2003207357-Al.
06-NOV-200
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22-MAY-2003.
(GETH ) GENENTECH INC.
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ADG04138 standard; protein;
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                                                                                                                        GETH ) GENENTECH INC.
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RESULT 698
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US2003207427-Al.
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US2003207350-Al.
                                                                  ADG62151 standard; protein; 250 AA. Novel human secreted and transmembrane US2003207428-A1.
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US2003096966-A1.
22-MAY-2003
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ADH03058 standard; protein; 2
Human secreted/transmembrane
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protein PRO1279

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Query Match
Best Local Similarity
RESULT 707
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ADH39092 standard;
Novel human secret
US2003096965-A1.
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Human secreted/transmembrane
US2003224478-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
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27-NOV-2003.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane
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20-NOV-2003
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Best Local Similarity
RESULT 713
ID ADH12129 standard; p
DE Novel human secreted
PN US2003207419-A1.
PD 06-NOV-2003.
RESULT 716
ID ADG812
DE Human
PN US2003
PD 16-OCT
PA (GETH
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ID ADG542
DE Novel
PN US2003
PD 06-NOV
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RESULT 71
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Best Local Similarity
RESULT 708
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06-NOV-2003.

(GETH ) GENENTECH INC.

(GETH ) 45.0%; {

Match 45.0%; {
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06-NOV-2003.
(GETH) GENENTECH INC.
(GETH) 45.0%;
Match 45.0%;
     Human PRO polypeptide #253. US2003194793-A1. 16-OCT-2003.
                                                                                                     ADG54279 standard; protein; 250 AA.

Novel human secreted and transmembrane
US2003207416-A1.
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Novel human secreted and transmembrane
US2003207414-A1.
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"Y Match 45.

"L Local Similarity 48.
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Novel human secreted and tra
US2003207421-A1.
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Novel human secreted and transmembrane
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(GETH ) GEN
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Novel human secreted and transmembrane
US2004006206-A1.
08-JAN-2004.
(GETH ) GENENTECH INC.
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US2003224984-A1.
04-DEC-200
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                                  ADH04489 standard; protein; i
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Human PRO polypeptide #253.
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                                     ADI29907 standard; protein; Novel human secreted and tra US2003096961-A1.
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Human secreted/transmembrane
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                                                                                                                                            Best Local Similarity RESULT 742
                                                                                                                                                                                 B B B I
                                                                                                                                                                                                                   RESULT 741
                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 740
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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Best Local Similarity
RESULT 737
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RESULT 736
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04-MAR-2004.

(GETH ) GENENTECH INC.

(GETH ) 45.0%; (45.0%; (48.2%; (48.2%))
                            ADM42594 standard; protein;
Human PRO polypeptide #253.
US2004058424-A1.
25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                      US2004.
26-FEB-2004.
(GETH) GENENTECH INC.
(GETH) GENENTECH 45.0%;
45.0%;
48.2%;
                                                                                                         Human PRO polypeptide #253. US200404833-A1.
                                                                                                                                                                                      ADJ65734 standard; protein;
Human PRO polypeptide #253.
US2004038335-A1.
                                                                                                                                                                                                                                                                                                                                  Human PRO polypeptide #104. US2004043927-A1. 04-MAR-2004
                                                                                                                                                                                                                                                         US2004044180-A1.
04-MAR-2004.
                                                                                                                                                                                                                                                                         ADK66662 standard; protein;
Human PRO polypeptide #93.
                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO polypeptide #253.
US2004038336-A1.
26-FEB-2004
                                                                                                                                                                                                                                                                                   ADK66662 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ63717 standard; protein;
Novel human secreted and tra
US2004039164-Al.
                                                                                                                                                                                                                                             GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI18436 standard;
Novel human secret
                                                                           Local Similarity
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 Local Similarity
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                                                                                            GENENTECH INC.
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secreted and transmembrane
INC.
45.0%;
Y 48.2%;
                                                                                                                                                  1 INC.
45.0%;
y 48.2%;
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48.2%;
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48.2%;
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48.2%;
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transmembrane
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No.
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                                                                         618.5; DB 8;
No. 8.7e-40;
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No.
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No. 8.7e-40;
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No.
8.7e-40;
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                                                                                                                                                 .5; DB 8;
8.7e-40;
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8.7e-
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e-40;
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QUETH ) GENENTECH 1
QUETY MATCH
Best Local Similarity
RESULT 745
ID ADM28456 of
DE Hour
           Best Loc
RESULT 753
                                                                                       Query Match
Best Local Similarity
RESULT 752
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Best Local Similarity
RESULT 751
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RESULT 748
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RESULT 747
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                                Query Match
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                                                                                                                             AAY42439 standard; |
CASB12 amino acid s
WO9949055-A1.
30-SEP-1999.
                                      02-JUN-2000.
(FUSO ) FUSO
                                                           WO200031257-A1.
                                                                      Human serine
                                                                                                                                                                                                                   ADS34892 standard; protein; 250 / Human autoimmune disease-related W02004083403-A2.
                                                                                                                                                                                                                                                                                                                                 10-SEP-2004.
10-SEP-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
45.0%;
ary Match
45.2%;
48.2%;
                                                                             AAB11712 standard;
                                                                                                                                                                                                                                                                                              ADR72890 standard; protein; 2 Human ovarian cancer-related WO2004075713-A2.
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ry Match 45.0%;
t Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                     ADR72632 standard; protein; 250 AA. Human renal cell carcinoma-related
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US2003207354-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI96490 standard;
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Human secreted/tra
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2003.
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45.0*
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                  Similarity
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  standard;
                                                                  ndard; protein;
protease BSSP6
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48.2%;
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45.0%;
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(hBSSP6)
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Pred.
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d tumour marker kallikrein
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e protein
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No. 8.7
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No.
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                                                                  SEQ
                  9.9e-40;
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8.7e-40;
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8.7e-40;
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8.7e-40;
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8.7e-40;
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8.7e-40;
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Best Local Similarity
RESULT 760
ID AAB36482 standard; p
DE Pusion gene with hum
PN W0200066709-A2.
PD 09-NOV-2000.
PA (ORTH) ORTHO-MCNEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See
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Best Local Similarity
RESULT 756
                                                                                                                             Best Local Similarity
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CASB12 polypeptide o
WO9949055-A1.
30-SEP-1999.
   AAY36093
Extended
                                                                                 AAB67542 standard; protein; 288 AA. Amino acid sequence of catalytic domain W0200116289-A2.
                                                                                                                                                                                   AAB36482 standard; protein; 288 AA.
Fusion_gene with human serine protease catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR72889 standard; protein; Human ovarian cancer-related W02004075713-A2.
                                                                                                                            (ORTH ) ORTHO-MCNEIL PHARM | 43.9%; t Local Similarity 51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human soft tissue sarcoma-upregulated WO2004048938-A2.
                                                                                                                                                                                                                    (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

'Y Match 44.6%; Score 612.5; DB 2;

Local Similarity 48.0%; Pred. No. 2.8e-39;
                                                                                                                                                                                                                                                                                                                                                            WO2004083403-A2.
                                                                                                                                                                                                                                                                                                                                                                                   ADS34893 standard; protein; 282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human renal cell WO2004077060-A2.
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Human kallikrein-11, marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A human prostate-associated WO9941387-A2.
                                                                                                                                                                                                                                                                                                                                     (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                       (MOUN ) MOUNT SINAI HOSPITAL.

CY Match 45.0%;
Local Similarity 48.2%;
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ry Match 45.0%;
t Local Similarity 48.2%;
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  standard;
human secr
                                                          ORTHO-MCNEIL PHARM INC.
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ard; protein; 250 secreted protein
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                                                                                                                                                                                                                                                                             protein; 281 AA.
derived from Expressed
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45.0%;
48.2%;
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51.1%;
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d tumour
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for prostate
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  sequence,
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No. 1.
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No.
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No. 9.9
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No. 9.9e-40;
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                marker
                                                                                                                             1.7e-38;
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9.9e-40;
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9.9e-40;
                                     .5; DB 4;
1.7e-38;
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9.9e-40;
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.9e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein1
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RESULT 765
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                                                                                                                                                                                                                                                                                        Novel
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Query Match
Best Local S
RESULT 763
                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                    Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1999.
(GEST ) GENSI
AAB67543 standard; protein; 289 ?
Amino acid sequence of catalytic
WO200116289-A2.
                                                                                         AAB36483 standard; protein; 289 AA. Fusion gene with human serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU82732 standard; I
Amino acid sequence
WO200200860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB11714 standard; protein; Human serine protease BSSP6 WO200031257-A1.
                                                                                                                                                                  Human kallikrein
WO2004029285-A2.
                                                                                                                                                                                      ADN10932 standard;
                                                                                                                                                                                                                                                    WO200214485-A2.
                                                                                                                                                                                                                                                                                                                                       Murine NOVX protein WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE GENOMICS INC.
ry Match 43.6%;
t Local Similarity 46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human protease, WO200208396-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE19166 standard; protein; 320
Human protease, PRTS-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FUSO ) FUSO PHARM IND LTD.
xy Match 43.7%;
t Local Similarity 44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP19401 standard;
Human secreted poly
US2004110939-A1.
                                                                                                                                             (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                          AAU79390 standard;
                                                                                                                                                                                                                                                                                                                             06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                           ADI17075 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2000
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                                                             (ORTH ) ORTHO-MCNEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUGE-) SUGEN INC.
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                                                                                                                                                                                                                                                              andard; protein; 2
kallikrein KLK15.
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polypeptide #
                                                                                                                                                                           d; protein; 256
15, marker of e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 3
e of novel
                                                                                                                                                                                                                                                                                                                                                           protein;
                                      L PHARM RES INC.
43.6%; Score 9
49.1%; Pred. 1
                                                                                                                                                                                                           43.6%;
                                                                                                                         43.6%;
                                                                                                                                                                                                                                                                                                                                                homologue
                                                                                                                                                                                                                                                                                             43.6%;
49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.6%;
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l human
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(hBSSP6)
                                                                                                                       Score
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Pred.
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                Score 599.5; DB 5; Pred. No. 3.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
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SeqID
                                                                                                                                                                            endocrine
        AA.
c domain
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                                                                                                                        599;
No. 2.
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                                       3.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5; DB 5;
3.3e-38;
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1.8e-38;
                                                                                           catalytic
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         ij
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.8e-38;
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.8e-38;
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         PFEK1-6XHIS-TAG
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RESULT 776
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Best Local Similarity
RESULT 772
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Human KLK-L6 protein #2. W0200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE08017 standard; protein; 2
Human PS133 consensus protein
US6232455-B1.
15-MAY-2001.
(ABBO) ABBOTT LAB.
                                                                           Pig pro-trypsin.
US2004043455-A1.
                                                                                                                                                           ABB98258 standard; protein;
Pig trypsinogen SEQ ID NO 1.
WO200261064-A2.
                                                                                            ADJ92132 standard;
                                                                                                             (HOFF) ROCHE DIAGNOSTICS GMBH.
(HOFF) HOFFMANN LA ROCHE & CO;
xy Match
t Local Similarity 45.6%; Pr
                                                                                                                                                                                                                                                                                                          AAB21312 standard;
Human TLSP.
WO200053776-A2.
                                                                                                                                                                                                               03-JAN-1997.
(NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                     WO9700316-A1.
                                                                                                                                                                                                                                            Porcine trypsinogen.
                                                                                                                                                                                                                                                      AAW08475 standard;
                                                                                                                                                                                                                                                                                                                                                                                            ADI17077 standard;
Human NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse serine protease BSSP6 W0200031257-A1.
                                                                                                                                                                                                                                                                                       (MOUN) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                          WO200268649-A2.
06-SEP-2002.
                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC31389 standard; protein;
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                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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th 43.5%;
Similarity 47.0%;
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                                      S BIOTECH INC.
41.7%; S
2y 45.6%; P
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homologue
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43.1%;
49.3%;
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45.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence
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; Score 598.5; DB 4;
; Pred. No. 3.5e-38;
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Pred.
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Score
Pred.
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e SeqID
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(mBSSP6)
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Pred.
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re 573; DB 5;
d. No. 2.8e-36;
                                       573;
No. 2.
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No. 8.
                                                                                                                                                                                              573; DB 2;
No. 2.8e-36;
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No. 6.
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No.
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No. 3.6e-38;
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40
                                       DB 8;
.8e-36;
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.7e-38;
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.8e-38;
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-38;
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Query
Best Loc
RESULT 789
ID ADL71'
DE Hum'
PN W'
PD
                                                                      Best Local Similarity
RESULT 788
ID ABO00554 standard; p
DE Novel human polypept
PN W02003023013-A2.
PD 20-MAR-2003
PA (HYSE-) HYSEQ INC.
                                                                                                                                                                                     Best Local Similarity
RESULT 787
ID AAR2177
                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 786
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RESULT 782
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Best Local Similarity
RESULT 781
                                                            Query Match
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                                                                                Novel human polypeptide #141. W02003023013-A2. 20-MAR-2009
            Human kallikrein 13
WO2004021009-A2.
                   ADL71094 standard; protein;
Human kallikrein 13 protein
                                                                                                                                                                   Human KLK-L4 protein WO200053776-A2.
                                                                                                                                               (MOUN ) MOUNT SINAI
                                                                                                                                                                            AAB21300 standard; protein;
Human KLK-L4 protein #2.
                                                                                                                                                           14-SEP-2000
                                                                                                                                                                                                                                               Antipsoriatic protein WO2004028479-A2.
                                                                                                                                                                                                                                                                  ADN05516 standard;
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                                                                                                                                                                                                                                                                                                                          Amino acid sequence WO2003033731-A2.
                                                                                                                                                                                                                                                                                                                                             ABR55400 standard;
                                                                                                                                                                                                                                                                                                                                                                                             ABP64969 standard; protein;
Human protein SEQ ID 629.
WO200259260-A2.
01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB21298 standard; pr
Human KLK-L3 protein
WO200053776-A2.
                                                                                                                                                                                                                                                                                                      (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ26666 standard;
Human protein modif
WO2003000844-A2.
                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ
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ITY Match

It Local Similarity 46.9%;
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Human kallikrein 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000
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ry Match 41.4%;
t Local Similarity 46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2003
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(MOUN ) MOUNT
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                                                 Similarity
                                                                    HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                   protein; 2
e of human
                                                                                                                           HOSPITAL.
41.3%;
46.8%;
                                                                                                                                                                                                                                                                protein;
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in #2.
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41.4%;
46.7%;
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4, marker of endocrine
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                                                 41.3%;
46.8%;
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46.7%;
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41.4%; (
46.9%; )
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                    277 AA.
SEQ ID NO:1.
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n kallikrein
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#924.
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                                                567;
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No. 9e-36;
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No.
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No.
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                                                ; DB 6;
9e-36;
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6.2e-36;
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RESULT 798
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RESULT 790
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Human secreted protein encoc
WO9935158-A1.
                                                                                                           AAY38426 standard; protein; 293
Human secreted protein encoded l
                                                                                                                                                                                                                                                                                                                                           AAY16777 standard; protein; 293 AA. Human keratinocyte derived protease W09918219-A1.
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                    WO9963088-A2.
                              Membrane-bound
                                       AAY66726 standard;
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WO9935158-A1.
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Local Similarity 46.8%;
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latic protein sequence #287
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                              ADA57425 standard; protein;
Human secreted protein #257,
WO2002102994-A2.
                                                                                                                           ABO17843 standard; protein; 293 AA. Novel human secreted and transmembrane US2003032156-A1.
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Human PRO polypeptide #96.
US2003027163-A1.
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WO200053776-A2.
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WO200109327-A2.
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Human PRO1132 (UNQ570) prote
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Human PRO1132 polypeptide sequence.
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Best Local Similarity
RESULT 815
ID ABU66797 standard; p
DE Human PRO polypeptid
PN US2003036180-A1.
PD 20-FEB-2003.
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ID ABU725
DE Novel
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                                                        ADA41303 standard; protein;
Human secreted protein.
W02002102993-A2.
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Human PRO polypeptide #228.
US2003036180-A1.
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Novel human secrete
US2003003531-A1.
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Human PRO1132 polypeptide.
US2002103125-A1.
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Human secreted/transmembrane pro
US2002160384-A1.
31-OCT-2002.
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Human secreted protein #257,
WO2002102994-A2.
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Human secreted protein #257.
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Query Match
Best Local Similarity
RESULT 826
ID ABU59438 standard; p
DE Novel human secreted
PN US2003027985-A1.
PD 06-FEB-2003.
                                                                                                                                                Best Local Similarity
RESULT 825
ID ABU92373 standard; p
DE Novel human secreted
PN US2003022187-A1
PD 30-JAN-2003
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27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
41.1%; Standard Sci Standard Secreting Sci Standard Secreting Sci Standard Secreting Secre
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12-SEP-2002.
(GETH) GENENTECH INC.
(GETH) GENENTECH 41.1%;
Match 41.1%;
45.3%;
ABU59438 standard; protein; 293 AA. Novel human secreted or transmembrane US2003027985 AAI.
                                                                                                                                                       Novel human secreted and transmembrane US2003022187-A1.
                                                                                                                                                                                                                                                                                                                                      US2002142961-A1.
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Human sectreted/transmembrane
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27-DEC-2002.
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20-FEB-2003.
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US2002127576-A1.
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Novel secreted and
US2003017563-A1.
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27-DEC-2002.
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Human PRO polypeptide #228.
US2003054517-Al.
20-MAR-2003.
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US2003073212-A1.
17-APR-2003
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US2002123463-A1.
05-SEP-200
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Human secreted and
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Novel human secreted and tra
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28-NOV-2002.
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US2003087350-A1.
08-MAY-2003
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                                                              ADA10293 standard; protein; ;
Human secreted/transmembrane
US2003059831-A1.
27-MAR-2003.
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                                                                                                                                             ADA21506 standard; protein; i
Human secreted/transmembrane
US2003054404-A1.
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Human PRO polypeptide #228.
US2003073215-A1.
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ADA67629 standard; protein;
Human PRO polypeptide #228.
US2003068795-A1.
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13-MAR-2003.
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Human secreted/transmembrane
US2003054359-A1.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein
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Human PRO polypeptide #228.
US2003082705-A1.
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Human PRO polypeptide #228.
US2003068794-A1.
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                                               ADB24815 standard; protein; i
Human PRO polypeptide SEQ ID
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24-APR-2003.
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(GETH ) GENENTECH INC.
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Human PRO polypeptide #228.
US2003082710-A1.
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01-MAY-2003.
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Human PRO polypeptide #228.
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US2003073211-A1.
17-APR-2000
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US2003082708-A1.
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Human PRO polypeptide #228.
US2003082703-A1.
01-MAY-2003.
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ADB25375 standard; protein; 2
Human PRO polypeptide SEQ ID
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Human PRO polypeptide #228.
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22-MAY-2007
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13-MAR-2003.
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Human PRO polypeptide #228.
US2003092147-A1.
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Human PRO polypeptide #228.
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                   ADA96040 standard; protein;
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US2003082709-A1.
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Human PRO polypeptide #228.
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         Human secreted/transmembrane US2003059782-A1.
                           ADA39291 standard; protein;
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Novel human secreted and transmembrane
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30-JAN-2003.
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Human PRO polypeptide #228.
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                              Novel human secreted and tra
US2003082689-A1.
01-MAY-2007
                                                                                                                                                                                                                                                        Novel human secreted and transmembrane US2003082766-A1.
                                                                                                                                                                                                                                                                                                                    ADB15496 standard; protein;
Human PRO polypeptide #228.
US2003087352-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane
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Novel human secreted and transmembrane protein
US2003082712-A1.
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Human PRO polypeptide SEQ ID
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24-APR-2003.
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(GETH ) GENENTECH INC.
(ALL%) 41.1%; (
                                       Human PRO polypeptide SEQ ID US2003077719-A1.
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Human PRO polypeptide SEQ ID
US2003077717-A1.
                                                                                                                                                                                                                ADB77416 standard; protein; 293 AA. Novel human secreted and transmembrane US2003082696-A1.
                                                                                                                                                                                                                                                                                                 ADB86811 standard; protein;
Human PRO polypeptide #228.
US2003082697-A1.
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Novel human secrete
US2003082764-A1.
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Novel human secreted and transmembrane
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ilarity 45.3%; Pred.
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                          ADC11487 standard; protein; Human secreted/transmembrane US2003069403-A1.
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10-APR-2003.
                                                                                                  Human secreted/transmembrane
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Human PRO polypeptide #96.
US2003064375-A1.
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Human secreted/transmembrane
US2003049681-A1.
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US2003027754-Al.
06-FEB-2003
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Novel human secreted and tra
US2003082692-A1.
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Human PRO polypeptide SEQ ID
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Human PRO polypeptide SEQ II
US2003077716-A1.
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08-MAY-2003.

(GETH) GENENTECH INC.

(GETH) 41.1%;

March 41.1%;

45.3%;
                                                                                                                                                                                          Novel human secreted and transmembrane US2003087361-A1.
                              US2003087363-A1.
                                                  Novel human
                                                   ADC54675 standard; protein; Novel human secreted and tra
                                                                                                                 Human PRO polypeptide #228.
US2003087362-A1.
08-MAY-2003
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Novel human secreted and tra
US2003087367-Al.
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US2003087366-A1.
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US2003087365-A1.
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-2003.
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41.1%;
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US2003087360-A1.
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Novel human secreted and tra
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US2003087364-A1.
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US2003194776-A1.
16-OCT-2003.
                   Novel human secreted and tra
US2003073090-A1.
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Novel human secreted and tra
US2002193299-A1.
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US2003194773-A1.
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ADD56240 standard; protein;
Human PRO polypeptide #96.
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Novel human secreted and transmembrane
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Novel human secreted and transmembrane US2003087304-A1.
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Human PRO polypeptide #228.
US2003199055-A1.
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US2003203428-A1.
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Human PRO polypeptide #228.
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Human PRO polypeptide #228.
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US2003199033-A1.
23-OCT-2003
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Human PRO polypeptide #228.
US2003203429-A1.
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Human PRO polypeptide #228.
US2003199064-A1.
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Human PRO polypeptide #228.
US2003199059-A1.
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                                                              ADG23247 standard; protein; 293 AA.
Novel human secreted and transmembrane
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Human PRO polypeptide #228.
US2003199031-A1.
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Human PRO polypeptide #228.
US2003207418-A1.
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(GETH) GENENTECH INC.
(BETH) 41.1%;
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ADH82019 standard; protein; 293 AA. Novel human secreted and transmembrane US2003207388-A1.
                                                                                  ADI63605 standard; protein; 293 AA. Novel human secreted and transmembrane US2003207387-A1.
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US2003207372-A1.
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Novel human secreted and tra
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                                                                          ADC81193 standard; protein; Novel human secreted and tra
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Local Similarity 45.3%; E
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(GETH) GENENTECH INC.
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15-MAY-2003.
(GETH ) GENENTECH INC.
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29-MAY-2003.
(GETH ) GENENTECH INC.
(GETH ) 41.1%;
Match 41.1%;
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US2003092110-A1.
15-MAY-John
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US2003092108-A1.
                             ADE89319 standard; protein;
Human PRO polypeptide #228.
US2003199062-A1.
                                                                                                  Human PRO polypeptide #228. US2003203439-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD86409 standard; protein;
Human PRO polypeptide #228.
US2003203440-A1.
30-OCT-2003.
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Human PRO polypeptide #228.
US2003211571-A1.
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23-OCT-2003.
(GETH ) GENENTECI
                                                                                                                ADF35030 standard; protein;
Human PRO polypeptide #228.
US2003199029-A1.
23-OCT-2003.
                                                     ADE92345 standard; protein; 293 AA.
Novel human secreted and transmembrane
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Human PRO polypeptide #228.
US2003199052-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                               שביים standard; protein; Human PRO polypeptide #228.
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Human PRO polypeptide #228.
US2003199061-A1.
23-OCT-2003.
(GETH) GENENTECH INC.
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Human PRO polypeptide #228.
US2003199027-A1.
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Human Pro polypeptide #228.
US2003194794-A1.
16-OCT-2003
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Best Local Similarity
RESULT 1042
ID ADE91793 ~*
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Best Local Similarity
RESULT 1050
ID ADCORD
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Best Local Similarity
RESULT 1049
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RESULT 1043
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06-NOV-2003.
(GETH) GENENTECH INC.
(GETH) 41.1%;
The Match 41.1%;
45.3%;
                                                Human PRO polypeptide #228. US2003208055-A1. 06-NOV-2003
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                                                                                                                             US2003207426-A1.
                                                                                                                                                                                                                                                                              Human PRO polypeptide #228. US2003207376-A1. 06-NOV-2003.
                                                                                                                                           ADG24351 standard; protein; 293 AA.
Novel human secreted and transmembrane
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Human PRO1132 polypeptide.
US2003228655-A1.
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Human PRO polypeptide #228.
US2003199063-Al.
23-OCT-2003.
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Best Local Similarity
RESULT 1054
ID ADG19568 stand-
DE Human PRO
PN US200
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West Local Similarity

RESULT 1051

ID ADF99257 stand

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Human PRO polypeptide #228.
US2003207357-A1.
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Human PRO polypeptide #228.
US2003207425-A1.
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Human PRO polypeptide #228.
US2003207375-A1.
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US2003207353-A1.
                                                             ADF97030 standard; protein;
Human PRO polypeptide #228.
US2003207371-A1.
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Human PRO polypeptide #228.
ADG06215 standard; protein;
Human PRO polypeptide #228.
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27-NOV-2003.
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US2003207351-A1.
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Best Local Similarity RESULT 1068
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Best Local Similarity
RESULT 1065
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US2003207423-A1.
06-NOV-2003
                                                                                ADG62101 standard; protein; 293 AA. Novel human secreted and transmembrane US2003207428-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
41.1%;
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ADG82302 standard; protein;
Human PRO polypeptide #228.
US2003207358-A1.
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Query Match
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RESULT 1072
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ADG81750 standard; protein;
Human PRO polypeptide #228.
US2003207805-A1.
06-NOV-2003.
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06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) 41.1%; (
41.1%; (
                                                                                                      ADG71563 standard; protein; 293 AA. Novel human secreted and transmembr
                                                                                                                                                                                                                                                                  ADG58093 standard;
Novel human secrete
US2003207363-A1.
                                                                                              US2003207421-A1.
                                                                                                                                                         06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                 US2003207415-A1.
                                                                                                                                                                                             Novel human
                                                                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane US2003207420-A1.
                                                                                                                                                                                                     ADG53677 standard;
                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG58645 standard; protein; 293 AA. Novel human secreted and transmembr US200320736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted and transmembrane US2003207364-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003207365-A1.
06-NOV-2003.
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(GETH ) GEN
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(GETH ) GEN
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                                                                                                                                                                                         undard; protein; 293 AA. secreted and transmembrane
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45.3%;
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45.38;
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No.
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No.
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No. 1.5e-35;
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No. 1.5
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No. 1.5e-35;
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No. 1.5e-35;
                                                  1.5; DB 8
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1.5e-35;
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. 1.5e-35;
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1.5e-35;
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. 1.5e-35;
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.5e-35;
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Query Match
Best Local Similarity
RESULT 1085
ID ADH12703 standard, p
DE Novel human secreted
PN US2003207378-A1.
PD 06-NOV-2003
PA (GETH ) GENENTECH IN
                                                                                                                          Best Local Similarity RESULT 1086
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Best Local Similarity
RESULT 1084
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RESULT 1079
ID ADDAGE
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RESULT 1078
ID ADH19555 standard;
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                                                                             ADH21048 standard; protein; ;
Human secreted/transmembrane
                                                                                                                                                                                                                                           ADH12703 standard; protein; 293 AA.
Novel human secreted and transmembrane
                                                                                                                                                                                                                                                                                                                                                                     US2003207366-A1.
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US2003207366-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO polypeptide #228. US2003194793-A1. 16-OCT-2007
                                                                                                                                                                                                                                                                                                                                                                                                                                ADG56437 standard;
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Novel human secreted and transmembrane
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US2003207414-A1.
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Human secreted/transmembrane
US2003228656-A1.
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45.3%;
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Pred. No. 1.5e-35;
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No. 1.5e-35;
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No. 1.5e-35;
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No. 1.5e-35;
                                                                                 PRO1132
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1.5e-35;
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1.5e-35;
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Match

Best Local Similarity

RESULT 1092

ID ADIS1245 stand

DE Human PRO
PN US200
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ID ADG5982
DE Novel h
PN US20032
PD 06-NOV-
                                                                                                                                                                                      RESULT
ID AD
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                                                                                                                                                                                               ADG09988 standard; protein; Novel human secreted and traUS2004009548-Al.
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Human PRO polypeptide #228.
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Novel human secreted and transmembrane
                             US2004009547-A1.
15-JAN-2004.
                                               ADG09336 standard; protein; 293 AA.
Novel human secreted and transmembrane
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22-APR-2004.
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Human PRO polypeptide #228.
US2004058424-A1.
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Human kallikrein 5
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                                                     Amino acid sequence WO200200860-A2.
                                                                                                                                                           ABG96356 standard; protein; Human ovarian cancer marker
                                                                                    AAU82729 standard;
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                                                                                                                                                                                        (MOUN) MOUNT SINAI HOSPITAL.

ry Match 41.0%;
t Local Similarity 45.9%;
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WO200053776-A2.
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Human NES1 polypeptide.
W09639175-A1.
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Human BS247 specific epitope.
WO9922027-A1.
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10-SEP-2004.

(MOUN) MOUNT SINAI HOSPITAL.
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(NEWE-) NEW ENGLAND
             Local Similarity
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Human renal cell ca
WO2004077060-A2.
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ry Match 41.1%;
Local Similarity 45.3%;
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Human PRO polypeptide #228.
US2003077659-A1.
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Query Match
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RESULT 1122
ID AAB21299 standard; p
DE Human KLK-L4 protein
PN W0200053776-A2.
PD 14-SEP-2000.
                     Best Local Similarity RESULT 1123
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RESULT 1121
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RESULT 1116
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AAB21309 standard;
Human KLK-L2.
                                                 14-SEP-2000.
(MOUN ) MOUNT SINAI
                                                                  Human KLK-L4 protein #1.
W0200053776-A2.
14-SEP-2000
                                                                                                                                                           Human KLK-L6 protein #1. W0200053776-A2.
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(MOUN ) MOUNT SINAI
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Human ovarian cancer-related tumour marker
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Human renal cell ca
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ry Match
t Local Similarity 45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer/angiogenesis/fibrosis-related W02003042661-A2.
                                                                                                                                                                                                                                                                                                                                               WO2004077060-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE40473 standard; p
Human kallikrein 10
WC2003070883-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EOSB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EOSB-) EOS BIOTECHNOLOGY INC
ry Match 41.0%; &
t Local Similarity 45.9%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2002102235-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovarian cancer-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                           MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EOS BIOTECHNOLOGY INC.
h 41.0%; Score
Similarity 45.9%; Pred.
                                                                                                                                                                                                                                                                                                                                                      d; protein; 276 AA carcinoma-related
         protein;
                             HOSPITAL.
40.9%;
49.1%;
                                                                                                                   HOSPITAL.
40.9%;
48.1%;
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45.9%;
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45.9%;
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45.9%;
         287
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                            Score
Pred.
                                                                                               256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AA.
D 2045)
                                                                                                                   Pred.
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Pred.
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Pred. No. 1.5e-35;
         A
                             561
No.
                                                                                                                                                                                                           564;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                               562;
                                                                                                                   No.
                                                                                                                                                                                                                                                                                               564; DB 8;
No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                       kallikrein 10
                                                                                                                                                                                                                                                                                                                                                                                       564;
No. 1
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No. 1.
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No. 1.
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                              25.
                             ; DB 3;
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.9e-35;
                                                                                                                                                                                                           DB 8;
.5e-35;
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.5e-35;
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.5e-35;
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.5e-35;
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RESULT 1125
ID AAB21310 standard;
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                                                                                                                          Query Match
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(ELIL ) LILLY & CO ELI.
(ELIC ) 40.8%; (
                                                            ADB80567 standard; protein; 244 AA. Ovarian cancer-associated protein # W0200210235-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        AAW22985 standard; protein;
Human serine protease 59 (SF
JP09149790-A.
                                                                                                                                                                   AAE37572 standard; protein;
Human 2047 protein.
                                                                                                                                                                                                                                        Human zyme.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                         Protease M, a novel WO9811238-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic shortened WO200261064-A2.
ADN39212 standard; protein; 244 AA.
Cancer/angiogenesis/fibrosis-related polypeptide,
                                                                                                                                              WO2003037258-A2.
08-MAY-2003.
                                                                                                                                                                                                                                                             AAB21323 standard;
                                                                                                                                                                                                                                                                                                                                             AAW51006 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyme APP-cleaving protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR44532 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB98259 standard; protein; 228 AA. Synthetic shortened trypsinogen SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOPF) ROCHE DIAGNOSTICS GMBH.
(HOPF) HOFFMANN LA ROCHE & CO AG F.
(Y Match
LOCal Similarity 46.7%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUN ) MOUNT SINAI HOSPITAL.
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Y Match 40.8%;
Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                     DAND ) DANA FARBER
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                                                   EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                   MILL-) MILLENNIUM PHARM INC.
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                                                                                                      Local Similarity
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                              ocal Similarity
                                                                                                                                                                                                                                                             protein;
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40.8%; Score 561;
46.7%; Pred. No.:
                                                                                                                                                                                                                                                                                                                                     serine
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                                                                                                               46.7%;
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                               46.7%;
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(SP59).
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No.
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No. 2.3e-35;
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No. 2
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2.3e-35;
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2.3e-35;
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2.1e-35;
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  NO:530
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Query Match
Best Local S
RESULT 1141
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RESULT 1138
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RESULT 1140
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RESULT 1137
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RESULT 1135
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RESULT 1134
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14-SEP-2000
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AAW05383 standard; protein;
Human amyloid precursor prot
WO9631122-A1.
                                                                                                   AAR67888 standard; protein; 253 AA.
Human stratum corneum chymotrophic
                                                                                                                                                                                                                                                                                        ABG96357 standard; protein;
Human ovarian cancer marker
                                                                                                                                                                                                                                                                                                                                                                      Human ovarian cancer-related WO2004075713-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR72624 standard; protein; 244 AA. Human renal cell carcinoma-related W02004077060-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ89076 standard; protein; 244 AJ
Human urological disorder related
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Human kallikrein 6 associated prote
US2004097452-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003042661-A2
22-MAY-2003.
                                                                   (SYMB-) SYMBICOM
                                                                               05-JAN-1995.
                                                                                         WO9500651-A1.
                                                                                                                                    (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 40.5%;
t Local Similarity 46.1%;
                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                            Human ovarian cancer WO200271928-A2.
                                                                                                                                                                                                                                                                                                                       (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 40.8%;
Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                                                              ADR72876 standard; protein;
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ry Match 40.8%;
t Local Similarity 46.7%;
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WO2004065576-A2.
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          protein
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No. 6.
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No. 5.7e-35;
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No. 2.
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No. 2.3e-35;
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.3e-35;
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.9e-35;
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.3e-35;
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10-OCT-1996

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Best Local Similarity
RESULT 1145
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RESULT
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RESULT 1143
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Best Local Similarity
RESULT 1142
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ADN39180 standard; protein;
                                                                                                   Human heat mitochondrial protein W02003087768-A2. 23-OCT-2003.
                                                                                                                                                                                                                                                                    ADB80484 standard; protein; 253 AA. Ovarian cancer-associated protein # WO2002102235-A2.
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Human SCCE protein |
WO200262135-A2.
15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                  WO2003029468-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein differentially regulated in W0200281638-A2. 17-0CT-2002.
                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR58471 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200281638-A2.
17-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU07440 standard; protein; Protein differentially regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU82740 standard; protein; 253 AA. Amino acid sequence of novel human W0200200860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SCCE protein
WO200262135-A2.
15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB84406 standard;
                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ORIG-) ORIGENE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EGEL/) EGELRUD (HANS/) HANSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
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                                                                                                                                                                                                                                    EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGENE TECHNOLOGIES
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                                                                           AGE
                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELI.
40.4%;
44.6%;
                                     40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 253 AA.
N-terminal fragment
                                                                                                                                                                                                  40.48;
                                                                                                                                                                                                                                                                                                                                            40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.4%;
                                                                           RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ein; 253 AA.
regulated in
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% %
   253 AA
                                   Pred.
                                                                                                                                                                                              Score
Pred.
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Pred.
                                                      Score
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Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC.
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Pred.
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Pred.
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Pred.
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Pred.
                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                         #24.
                                 555;
No. 6.
                                                                                                                                                                                                555;
No. 6.
                                                                                                                                                                                                                                                                                                                                            No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555;
No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555;
No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555;
No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555;
No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555; DB 5;
No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          555; DB 2;
No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate
                                                                                                                                         therapeutic
                                                                                                                                                                                                                                                                                                                                          5; DB 6;
6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                   DB 7;
.9e-35;
                                                                                                                                                                                                DB 7;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 9е.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ı
                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IJ
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                                                  Length
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                                                                                                                                         target SeqID639
                                                                                                                                                                                                                                                                                                                                                                                                                               cancer clone 01676P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253;
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Best Local Similarity
RESULT 1155

ID ADN62898 standard; pl
DE Human NOVU8b.
PN US200403B223-A1.
PD 26-FEB-2004.
PA (MILL) MILLET I.
PA (SWIT/) SMITHSON G.
PA (KEKU) KEKUDA R.
PA (KEKU) KEKUDA R.
PA (JUJJ) JU J.
PA (PATT/) PATTURAJAN M
PA (SPTT/) PATTURAJAN M
PA (SPTT/) PATTURAJAN K.
PA (ELLE/) ELLERMAN K.
PA (ELLE/) ELLERMAN K.
PA (ELLE/) ELLERMAN K.
PA (ELLE/) ZENTANKAR U |
PA (ORTY/) OGT T.
PA (ORTY/) CATTERTON D W
PA (ZHOM/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STOM/) STONE D J.
PA (SHEM/) SHENOY S G.
PA (SHEM/) SHENOY S G.
PA (SHEM/) SHENOY S G.
PA (RAGEE/) LEACH M D.
PA (AGEE/) BERGHS C.
PA (BERG/) BERGHS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
RESULT 1151
ID ADL06515
DE Human tum
PN WO2004016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
RESULT 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
RESULT 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WOZUWYCZ
08-APR-2004.
(GETH) GENENTECH INC.
(GETH) GENENTECH 40.4%; /
MATCH 44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA05734 standard;
Human NOV18b prote
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR72880 standard; protein; 2
Human ovarian cancer-related
WO2004007713-A2.
10-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN04182 standard; protein; 253 AA. Antipsoriatic protein sequence #286. WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL06515 standard; protein; Human tumour-associated ant:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004016225-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL06515 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer/angiogenesis/fibrosis-related polypeptide, WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
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                                                                                                                                                                                                                  PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURAGEN CORP.
                                                                                                                                                                   ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein SEQ ID
                                                Z Þ
                                                                                                                                                                                                                                                                   z
                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOSPITAL.
40.4%;
44.6%;
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                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                        46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ein; 253 AA.
antigenic target
                                                                                                                                                                                                                                                                                                                                                                                                 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AA
NO:94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour marker kallikrein
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555;
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                                                                                                                                                                                                                                                                                                                                                                                                                        553
No.
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No. 6.
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No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                       .5; DB
9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
.9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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RESULT 1157
I ADMAC29
DE HUMBAN NU
PN US20040
PN US20040
PN (SEXM)
PA (MILL/)
PA (KEKU/)
PA (GOX/)
RESULT 1160
ID AAY9192
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 44.8%;
RESULT 1158
ID AAY77494 standard; protein;
                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1156
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                     Bovine trypsinogen WO200005384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY08025 standard; protein; Mouse protease-related proteE19736198-C1.
                                                                                                                                       AAR53638 standard;
Bovine trypsinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN62896 standard;
AAY91926 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                            (GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS2004038223-A1.
                                                                                                                                                                                                                                               PROD-) PRODIGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U/) MILLET I.
W/) PEYMAN J A.
U/) KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                               TILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMITHSON G.
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EISEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MALYANKAR U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTERTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZHONG M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDINGER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽.
                                    ELI.
40.2%;
47.5%;
                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.3%;
                                                                                                                                                                                                   40.2%;
                                                                                                                                                                                                                                                                                                                                                                       40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tein; 253 AA.
protein (PVP)
                                                                                                                                                                                                                                                                                                                                229 AA
                                    Score 552;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 553.5;
Pred. No. 9e-
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Pred.
                                                                                                                                                                                                                                                                                                                                                                       No. 9.
                                                                                                                                                                                                        552;
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No.
                                      1.1e-34;
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9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5; DB
9e-35;
                                                                                                                                                                                                        DB 3;
.1e-34;
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.8e-35;
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Query Match
Best Local S
RESULT 1164
                                                                                                Best Local Similarity RESULT 1168
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RESULT 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELII) LILLY & CO ELI.

Query Match
40.2%;
Best Local Similarity 46.3%;
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine SCCE protein N
W0200362135-A2.
15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                      AAU17043 standard; protein; 247 AA. Human novel secreted protein, SEQ ID WO200155441-A2.
                                                                                                                                                                                                                                              AAU23752 standard; protein; 247 AA. Novel human enzyme polypeptide #838. W0200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAB35701 standard;
Human trypsin hL ar
JP2000253887-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant trypsin. WO200017332-A1. 30-MAR-2000.
                                                                Connective tissue US2003054375-A1.
                                                                                                                                                                                                                      02-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                   AAU86677 standard; protein; 247 AA. Novel human connective tissue related
                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-2000.
(TTPH-) TT PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV18a protein WO2003029424-A2. 10-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB80953 standard; protein; Bovine met-phe-trypsinogen. WO200119970-A2.
AAW81767 standard; peptide; 223
                                                                                        ADB60011 standard;
                                                                                                                                 02-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                       WO200155343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001.
(ELIL) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
ry Match 39.8%;
t Local Similarity 46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB84420 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA05732 standard;
                                                                                                                                                                                                 Local Similarity
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                     Similarity
                                           HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                           hL amino
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Ç
                                                                           ; protein; 247
antigen (CTA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
in SEQ ID
                   39.8%;
46.1%;
                                                                                                          39.8%;
46.1%;
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46.1%;
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46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AA.
sequence.
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NO:92.
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                   Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                            #243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment
                                                                                                             547.5; DB 4;
No. 2.6e-34;
                                                                                                                                                                                                    547.5; DB 4;
No. 2.6e-34;
                                                                                                                                                                                                                                                                                             547.
                                                                                                                                                                                                                                                                                                                                                                                    549.5; DB 3;
No. 1.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550
No.
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No. 1
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No. 1.1e-34;
                     547.5; DB 7
No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                  polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5e-34;
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                                                                                                                                                                                                                                                                                             ; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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.2e
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                                                                                                                                                                                                                                                                                                        247;
                                                                                                                                                                                                                                                                                                                                                                                                 247;
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Bovine TRYP peptide

fragment

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Best Local Similarity
RESULT 1175
ID AAV91925 standard; p
DE Trypsinogen analogue
PN w0200017332-A1.
PD 30-MAR-2000.
RESULT 1178
                                                                                                                       PA DE DE
                                                                                                                                                                           Best Local Similarity RESULT 1176
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1173
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RESULT 1172
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Best Local Similarity
RESULT 1170
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Best Local S
ESULT 1171
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30-MAR-2000.
(ELIL ) LILLY & CO ELI.
(STIL ) 39.8%;
Match 39.8%;
                                                                                      04-NOV-2003.
04-NOV-2003.
(UYAR-) UNIV ARKANSAS MEDICAL
(UYAR-) UNIV ARKANSAS MEDICAL
39.7%; S
ery Match
45.8%; I
                                           Human protease m (Protm).
US2003199010-A1.
23-OCT-200
                                                                                                                                         Human protease US6642013-B1.
                            (UYAR-) UNIV ARKANSAS.
                                                                                                                                                 ADI39734 standard; protein; 244 AA.
Human protease M (proM) protein.
                                                                                                                                                                                                                                 Trypsinogen analogue. WO200017332-A1.
                                                                                                                                                                                                                                                     AAY91925 standard; protein;
                                                                                                                                                                                                                                                                                                                       AAR53637 standard;
Bovine trypsin.
EP597681-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Cationic bovine trypsinogen WO2003040093-A2.
                                                                                                                                                                                                                                                                                                 18-MAY-1994.
(ELIL) LILLY &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC73287 standard; protein;
Bovine 2PTC E protein - SEQ
WO2003060765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1999.

02-DEC-1999.

(MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.

39.8% Score 547; DB

37.7 Match

39.8% Fred. No. 2.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD35545 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG31841 standard;
Example protein #3
                                                                                                                                                                                                                                                                                                                                                                                       (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO (UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MITU ) MITSUBISHI (UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example protein WO200257954-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY69973 standard;
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       Local Similarity
                    Match
                                                                                                                                                                                                                                                                                          Match
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                                                                                                                                                                                                                                                                          39.8%;
46.1%;
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                                                                                                                                                                                                                                                                                                                                             protein;
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used in t
    39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 223
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46.1%;
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39.8%;
46.1%;
                                                                       244
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TRY1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           three-dimensional structure analysis method.
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ID 13.
                                                                                                                                                                                                                                                                                                                                              224
    Score 546; DB 8;
Pred. No. 3.3e-34;
                                                                                            Score 546;
Pred. No. 3
                                                                                                                                                                                    Score
Pred.
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Pred.
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Pred.
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Score 547; DB 2;
Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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Pred.
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                                                                                                                    SCI.
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                                                                                                                                                                                   547; DB 3;
No. 2.6e-34;
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No. 2.
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No. 2
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No. 2.
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No. 2.5e-34;
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                                                                                             DB 8;
                                                                                                                                                                                                                                                                           DB 2;
.5e-34;
                                                                                                                                                                                                                                                                                                                                                                 DB 7;
.5e-34;
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.5e-34;
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.5e-34;
              Length
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               244;
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Best Local Similarity
RESULT 1182
ID AAY78975 standard; p:
DE Canine anionic tryps:
PN W020009739-A1.
PD 24-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 1179
ID ADARSTO
                                                                                                                                Query Match
Best Local Similarity
RESULT 1181
                                                                                                                                                          Query Match
                                                                             Query Match
                                                                                                     AAB98502 standard; pro
Human Stratum Corneum
WO200129056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV18f.
US2004038223-A1.
26-FEB-2004.
(SMIT/) SMITHSON
(MILL/) MILLET I.
                                                                                       (UYAR-) UNIV
                                                                                                                                                         (RIEG/)
(SPAD/)
                                                                                                                                                                                  (DIPI/)
                                                                                                                                                                                                            (AGEE/
                                                                                                                                                                                                                           (SHEN/
(SHIM/
(ROTH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA05742 standard; protein; 247 AA.
Human NOV18f protein SEQ ID NO:102.
W02003029424-A2.
10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                               (ZHON/
                                                                                                                                                                                                                                                                                                                                                                 (LILL/)
(GUOX/)
(PATT/)
(SPYT/)
(EDIN/)
                                                                                                                                                                                                                                                                                                                                                                                                           (PEYM/)
(KEKU/)
(JUJJ/)
                                                                                                                                                                                                    (BERG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN62906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FUJY ) FUJI YAKUHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78974 standard;
Canine cationic try
WO200009739-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                      ) GANGOLLI E A.
) RIEGER D K.
) SPADERNA S K.
                                                                                                                                                                                 LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
FUJI YAKUHIN KOGYO KK.
h 39.7%; S
Similarity 44.2%; P
                                                                                                                                                                                                                                  PENA C E
SHENOY S
SHIMKETS
                                                                                                                                                                                                                                                           MILLER C E.
RASTELLI L.
STONE D J.
                                                                                                                                                                                                                                                                                                           GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                         EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
ORT T.
                                                                                                                                                                                                                                                                                                                                                                       GUO X.
PATTURAJAN M.
SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                  MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHSON MILLET I.
                                                                                                                                                                                                                                                                                                         ZHONG M
                                                                                                                                                                                                                                                                                                CATTERTON E.
                                                                  V ARKANSAS.
39.7%;
ilarity 46.5%;
                                          ard; protein;
trypsinogen a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rd; protein;
trypsinogen
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                                                                                                             protein; 225 AA.
eum Chymotryptic
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                                                                                                                                       39.7%;
45.5%;
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39.7%;
45.6%;
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45.5%;
                                          amino
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Score
Pred.
                                                  246
Score 545; DB 3;
Pred. No. 4e-34;
                                                                   Score
Pred.
                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AA.
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 546; DB 6;
Pred. No. 3.3e-34;
                                          AA.
o acid
                                                                   545;
No. 3.
                                                                                                                                      546; DB 8;
No. 3.3e-34;
                                                                                                             Enzyme,
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No. 3.3e-34;
                                        sequence
                                                                   DB 4;
.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                             SCCE,
        Length
                                                                                                                                              Length 247;
                                                                          Length
                                                                                                             catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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         246;
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AJINOMOTO

AJINOMOTO

AJINOMOTO

MATCH

Best Local Similarity

RESULT 1187

ID ADI16686 stan<sup>2</sup>

DE Human NOV"

PN WO20°
                                                                              RESULT ID AIR DE HILD AIR DE H
Best
RESULT
ID AE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN 1998.

(BGHM ) BRIGHAM & WOMENS HOSPITAL.

IYY MARCh

39.5%; Score

44.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN42340 standard; protein;
Human novel proteinNOV 62.
US2004033493-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC73299 standard; protein; 220 AA. Stereostructure-related 2PTC_E protein. WO2003060765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW64260 standard; protein; 246 AA.
Human amyloid beta-protein precursor inhibitor.
W09824886-A1.
ABB78122 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stereostructure-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC73301 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB21326 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TCHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003060765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            TCHERNEV V T.
SPYTEK K A.
ZERHUSEN B D.
PAITURAJAN M.
PAIMKETS R A.
                                                                                                                                                          MILLER C E.
GERLACH V.
TAUPIER R J.
GUSEV V Y.
COLMAN S D.
WOLENC A R.
PENA C E A.
PURTAK K.
GROSSE W M.
                                                                                                   ALSOBROOK J P.
LEPLEY D M.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                      PADIGARU
ANDERSON
                                        Similarity
                                                                              BURGESS C
                                                                                                                                                                                                                                                                                                                                                                                                            GANGOLLI
                                                                                                                                                                                                                                                                                                                                                RASTELLI
                                                                                                                                                                                                                                                                                                                                                                 D X E
                                                                                                                                                                                                                                                                                                                 ្នែក
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.6%;
                                      39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2PTC
  223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 AA.
human pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 544;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                      Score 539.5; DB 8 Pred. No. 1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539.5;
No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541;
No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543;
No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541; DB 7;
No. 7.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 3;
5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259;
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Query Match
Best Local S
RESULT 1195
                                                                                  Best Loca
RESULT 1197
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RESULT 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1193
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Best Local Similarity
RESULT 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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Best Local Similarity
RESULT 1190
Query Match
Tocal Similarity
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                    ADL15205 standard; protein; Pancreatic kallikrein #1. CN1384199-A.
                                       WO200255702-A2.
18-JUL-2002.
                                                                                                                                                                                                                                                                                                             ABB84423 standard; peptide; 249 AA. Murine SCCE protein N-terminal fragment W0200262135-A2.
                                                            ABG70276 standard; protein; 247 Human Serine Protease TLSP-like
                                                                                                                                                                                                               ABR96164 standard; protein;
Human NOV13a protein SEQ ID
WO200290568-A2.
14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW64261 standard; protein; a
vallikrein substrate binding
                                                                                                                                                                                                                                                                                                                                                                                                             Kallikrein sul
WO9824886-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISB ) JAPAN TOBACCO INC.
ry Match 38.2%;
t Local Similarity 45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engraulis japonicus JP2001269173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB04644 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine SCCE protein WO200262135-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Partial trypsin sequence. US2002035434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FUIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence US2002072863-A1.
                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                        (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EGEL/) EGELRUD (HANS/) HANSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB84419 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FUIT ) FUJITSU LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB83322 standard; protein;
                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                           REMIN HOSPITAL SHENZHEN CITY.
h 37.8%; Score 519;
Similarity 44.5%; Pred. No. 3
                              CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUJITSU LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trypsinogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of trypsin.
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                                                                                                                                                                                37.8%;
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43.0%;
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43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%;
         37
42
         56
                                                                                                                                                           232
                                                                                                                                                                                                                                    261 AA
NO:70.
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g site.
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Pred.
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Pred.
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Pred.
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Pred.
                                                                                                                                                                                Score 519.5; DB 6; Pred. No. 3.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 531.5; DB 5; Pred. No. 4.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 538;
Pred. No. 1.
         Score 516;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
(aTry
                                                           protein
                                                                                                                                                                                                                                                                                                                                                                e 524;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        525;
No. 1.
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                                                                                            3.8e-32;
                                                                                                                                                                                                                                                                    2.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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         DB 5;
.9e-32;
                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -32;
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                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240;
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Query Match
Best Local Similarity
RESULT 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1203
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RESULT
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Best Local S
RESULT 1199
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RESULT 1202
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                                                                                                                                                                                                                                                                                                          01-JUL-2004.

01-JUL-2004.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(SINO-) SINOGENOWAX CO LTD CHINESE NAT HUMAN GEN.

(SINO-) SINOGENOWAX CO LTD CHINESE NAT HUMAN GEN.

(SINO-) SINOGENOWAX CO LTD CHINESE NAT HUMAN GEN.

(SINO-) SINOGENOWAX CO LTD CHINESE NAT HUMAN GEN.
                                                    Human KLK-L1 protein #2. WO200053776-A2. 14-SEP-2000
                                                                                                      O2-JUN-2000.
O2-JUN-2000.
(FUSO) FUSO PHARM IND LTD.
(FUSO) at the sery Match 36.4%;
ery Match 43.5%;
                                                                                                                                                        Human neurosin amino acid sequence. WO200031284-Al.
                                                                                                                                                                                                                                                                    ABR41530 standard; p
Human DITHP protein
WO200297031-A2.
                                                                                                                                                                                                                                                                                                                                                                                      ADQ30589 standard; prote:
Pancreas cancer marker -
WC2004055519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human protein WO2004038003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN04140 standard; protein; 247 AA. Antipsoriatic protein sequence #265. W02004028479-A2. 08-APR-2004. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN99594 standard; protein; 247 AA.
Novel human protein sequence #410.
Local Similarity
1207
                                                                                                                                                                                                                                                                                                                                                                                                                                     (FIVE-) FIVE PRIME THERAPEUTICS INC

ry Match 36.5%; Score :

t Local Similarity 43.3%; Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU87693 standard; protein; 247 Human pancreatic tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU87693 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Engraulis japonicus JP2001269173-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB04645 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9842849-A1.
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Human kallikrein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE PHARM
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                INCYTE GENOMICS INC. 36.5%; Similarity 43.3%;
                                  MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENENTECH INC.
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        HOSPITAL.
36.2%; ;
43.1%;
                                                                                                                                                                                                                                                                            protein; 261 AA.
n modification/maintenance protein.
                                                                                                                                                                                                                                                                                                                                                                                                              protein; 247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.5%;
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43.3%;
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trypsinogen
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37.4%;
46.4%;
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36.7%;
45.9%;
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                                                                                    254
        Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 9.8e-31;
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Pred. No. 1.1e-31;
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         498;
No. 1.
                                                                                                                                                                                                                 501;
No. 1
                                                                                                            500; DB 3;
No. 1.1e-30;
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No. 9
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         DB 3;
.7e-30;
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.8e-31;
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.8e-31;
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.6e-31;
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                   Length
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                    254;
                                                                                                                        223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   247;
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Best Local Similarity
RESULT 1208
ID AAU69819
   Query Match
Best Local Similarity
RESULT 1211
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RESULT
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1210
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                          (HOUG/)
(DBAS/)
(FOYT/)
                                                                                                                     ABB95279 standard; protein;
Human P703P putative full le
US2002022248-A1.
21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                 ABU71710 standard; protein; 254 AA. Prostate cancer specific antigen P703P #7. US2002192763-A1.
                                                                                                                                                                                                               (HEND
                                                                                                                                                                                                                                                                                                                                                                                                           AAG99059 standard, protein,
Human prostate-specific ami
WO200134802-A2.
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acid
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No. 1.7e-30;
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RESULT 1214
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RESULT 1213
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ry Match 36.2%; Score 
t Local Similarity 43.1%; Pred.
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Human KLK4 protein
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TY Match 36.2%; Score
Local Similarity 43.1%; Pred.
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  HENDERSON
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SEQ ID NO:13.
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.6e-30;
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.7e-30;
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Query Match
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RESULT 1221
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                                                                                                                           ADL27345 standard; peptide; 280 AA. Amino acid sequence of trypsinogen. WO2004019878-A2.
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(HOUG/)
(DBAS/)
(FOYT/)
                                     Amino acid seque WO2004019878-A2.
                                               ADL27346 standard; peptide; 461 AA.
Amino acid sequence of trypsinogen-0aa-sp55
                                                                                             (COMP-) COMPOUND THERAPEUTICS (AFEY/) AFEYAN N B.
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"G/) HOUGHTON R L.

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") FOY T M.

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BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
BDINGER S R.
GUNTHER B.
MILLET I.
SCIORE P.
SCIORE P.
LLERMAN K.
MACDOUGALL J R.
SMITHSON G.
         COMPOUND
AFEYAN N
                                                                                                                                                                                                                                                                                                                        SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                 Similarity
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                                              sequence
         THERAPEUTICS B.
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                                                                                                         INC.
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No. 2.1e-30;
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No. 1.7e-30;
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No. 1.7e-30;
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Best Local Similarity
RESULT 1230
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Query Match
Best To Service S
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W0200200867-Al.

03-JAN-2002.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

(SMIK ) SMITHKLINE 36.2%; Score 497; J

36.2%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Human prostase WO200104143-A2. 18-JAN-2001.
                                                                                                                                                                                                    AAW60592 standard; protein; 248 AA. Human prostate-specific kallikrein WO9820117-AI.
                                                                   AAY72524 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein sequence of prostase homologue W0200200708-A2. 03-JAN-2002.
                                                                                                                                                            (INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74932 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostase antigen WO200104143-A2. 18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOUN) MOUNT SINAI HOSPITAL.

12 Match 36.2%;

14 Local Similarity 43.1%;
                                                                                                                                                                                     4-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY72525 standard; protein; 254
Human prostase antigen #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostase. WO200053776-A2.
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

TY Match 36.2%; Score 497; DB 5;

Local Similarity 43.1%; Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB21320 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostase. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB21307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI.27348 standard; peptide; 485 AA. Amino acid sequence of trypsinogen-20aa-sp55. WO2004019878-A2. 11-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COMP-) COMPOUND
(AFEY/) AFEYAN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid seque
WO2004019878-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL27347
                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
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                                          antigen #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERAPEUTICS INC. B.
                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 254
e of prostase
                                                                                                          4 INC.
36.1%;
43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I HOSPITAL.
36.2%;
43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; 464 AA.
e of trypsinogen-3aa-sp55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%;
43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.2%;
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                                                                248 AA
                                                                                                        Score
Pred.
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Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 497; DB 4;
Pred. No. 2.1e-30;
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Pred.
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Pred.
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protein
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                                                                                                        496.5; DB 2;
No. 2.2e-30;
                                                                                                                                                                                                                          (HPSK)
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No. 2
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No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497.5; DB 8;
No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497
No.
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                                                                                                                                                                                                                                                                                                  DB 5;
.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                fragment
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                                                                                                                                                                                                                          protein
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standard;

protein;

254

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Best
RESULT
ID AF
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Best Local S
RESULT 1239
                                                                                                                      Best Local Similarity RESULT 1240
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RESULT 1234
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Best Local Similarity
RESULT 1233
ID AAU74770 standard;
                                                                                                                                            Query Match
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                                                                               Pancreas cancer marker - trypsin WO2004055519-A2.
                                                                                                     ADQ30588 standard; protein;
                                                                                                                                                                   ABR54241 standard; protein;
Human NOV35c protein SEQ ID
WO2003023001-A2.
                                           (HOFF ) HOFFMANN LA (SINO-) SINOGENOMAX
                                                                                                                                                                                                                                                                  ABR54239 standard; protein;
Human NOV35a protein SEQ ID
WO2003023001-A2.
                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                         (MOUN ) MOUNT SINAI HOSPITAL.

TY Match

Local Similarity 41.9%;
                                                                                                                                                                                                                                                                                                                                                                           Human trypsinogen. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                AAB21321 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOR-) BIOREXIS PHARM CORP.

ry Match 36.0%;
Local Similarity 41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR90673 standard, protein; 246 AA. Human trypsinogen partial protein. W02004078777-A2.
              Local Similarity
1241
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
36.1%; Score 496.5;
217 Tocal Similarity 43.4%; Pred. No. 2.7
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(TSUC/) TSUCHIHASHI Z.
(HUIL/) HUI L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kallikrein
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WO200200867-A1.
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Protein sequence of prostase
WC200200708-A2.
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                                                                                                                                                                                                                              Local Similarity
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                   A ROCHE & CO AG F.
X CO LTD CHINESE NA
36.0%; Score 49
41.9%; Pred. No
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36.1%; Score 496.5;
43.4%; Pred. No. 2.:
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                                                                                                                              36.0%;
41.9%;
                                                                                                                                                                                                                              36.0%;
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43.4%;
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NO:150.
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NO:146.
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Pred. No. 2.2e-30;
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494
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No.
                                                                                          precursor.
                                                                                                                              494.5; DB 6
No. 3.1e-30;
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No. 3.1e-30;
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No. :
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No.
                   F HUMAN GE
1.5; DB 8
3.1e-30;
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3.1e-30;
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3.1e-30;
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3e-30;
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y Match

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yest Local Similarity

RESULT 1243

ID AAG99058 standa

DE Human prost

PN W020013
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    Best Local Similarity
RESULT 1242
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                     ABB95278 standard; protein; 254 AA.
Human P703P mature protein SEQ ID NO 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU71709 standard; protein; Prostate cancer associated I US2002192763-A1.
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Human prostate cDNA encoded
                                                                                                                                                                                                                                                             (XUJJ/) XU J.
(DILL/) DILLON D C.
(MITC/) MITCHAM J L.
(HARL/) HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cDNA WO200173032-A2.
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                                                                                                                                                                  TOLS)
                                                                                                                                                                                                                                                                                                                                                                    JS2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
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CARTER D.
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WANG A.
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HEPLER W T.
HENDERSON R A.
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DAY C H.
VEDVICK T S.
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KALOS M D.
FANGER G R.
RETTER M W.
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DAY C H.
VEDVICK T S.
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KALOS M D.
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HEPLER W T.
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HARLOCKER S L.
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42.7%;
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42.7%;
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42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.0%;
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 AA.
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 494;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494;
No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494; DB 4;
No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494; DB 4;
No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o
f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254;
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Query Match
Best Local S
RESULT 1246
                                                   Query Match
Best Local Similarity
RESULT 1253
                                                                                                                      PA PA PA
                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1251
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1247
                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                             Human pancreatic kallikrein. (N1384199-A. 11-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate-specific poly US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR54390 standard; protein;
Prostate tumour specific pro
WO200289747-A2.
                  ADQ39654 standard;
Human myocardial ir
WO2004058052-A2.
                                                                                                                                                                                     Human kallikrein
US2004033582-A1.
                                                                                                                                                                                                                                (REMI-) REMIN HOSPITAL SHENZHEN CITY.

ry Match
t Local Similarity 40.4%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human mature pro
US2003185830-A1.
02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                   ABG76996 standard; protein; 262 AA.
Human kallikrein protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 36.0%;
t Local Similarity 40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB21319 standard;
                                                                                                                                                                                                            ADL64969 standard; protein;
                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB
(TSUC/) TSUCHIHASHI Z.
(HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                           WO200261131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB13973 standard;
                                                                                                                                           (EDMO/) EDMONDS M.
(HUIL/) HUI L.
(PERR/) PERRONE M.
                                                                                              POWELL J R.
RAMANATHAN C S.
SWANSON B.
TSUCHIHASHI Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORIXA CORP.
APPLERA CORP
                                                                                    ZERBA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ndard; protein;
prostate speci:
                               d; protein; 262 AA. infarction-associated
                                                                                                                                                                                               protein (KLK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                              36.0%;
                                                                                                                                                                                                                                                                                                                        36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.0%;
42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ein; 254 AA.
polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
                                                                                                                                                                                                            262 AA.
                                                                                                                                                                                                                                                                                                    262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 AA
                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 494; DB 7;
Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                  Score 494;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                       Score 494;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 494; DB 3; Pred. No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 494; DB 7; Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 494;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                              No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494; DB 6;
No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #59.
                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P703P
                                                              DB 8;
.6e-30;
                                                                                                                                                                                                                                  DB 7;
.6e-30;
                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                               derived protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H
                                                                                                                                                                                                                                                                                                                                   Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                        Length
                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254;
                                SEQ ID
                                1317
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/ INCYTE PHAN Match Local Similarity RESULT 1261 ID ABP74711 stand-DE Human glade PD WO200
                                                                   Best Local Similarity RESULT 1262
                                                                                                                                                                                                                                    Best Local Similarity RESULT 1260
                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1259
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1255
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                         ADL15204 standard; protein; Pancreatic kallikrein #1.
                                                                                                            Human glandular kallikrein 1
WO200281646-A2.
                                                                                                                                                                                                AAW71005 standard; protein, 262 AA. Human prostate-associated kallikrein W09832865-A1.
                                                                                         (CTLI-) CTL IMMUNOTHERAPIES
                                                                                                                                                                                                                                                           (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                    WO200053776-A2.
                                                                                                                                                                                                                                                                                               AAB21324 standard; protein; 258 AA.
Human EMSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACZUCCIO
14-SEP-2000.
14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
(MOUN) MOUNT SINAI HOSPITAL.
35.9%;
35.9%;
35.9%;
42.6%;
                                                                                                                                                                                                                                                                                                                         (MOUN ) MOUNT SINAI HOSPITAL.

ry Match 35.9%;
t Local Similarity 42.8%;
                                                                                                                                                                                                                                                                                                                                                                     Human EMSP.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                       AAB21308 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN04297 standard; protein; 247 AA. Antipsoriatic protein sequence #343 WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human trypsinogen. WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB21316 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS34891 standard; protein; 262 Full Human autoimmune disease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human trypsinogen
WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-2004.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR54277 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004083403-A2.
                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  284,
284,
2004
) GENENTECH INC.
35.9%;
42.1%;
REMIN HOSPITAL SHENZHEN CITY.
h 35.9%; Score 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; protein; 240 AA.
protein SEQ ID NO:341.
                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                        4 INC.
35.98;
40.48;
                                                                        35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                         35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.9%;
42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%;
                                                                       S CORP.
Score
Pred.
                                                      262
                                                                                                                                     262 AA.
                                                                                                                                                                                                                                                                                                                                                                                         253
  Score 493;
                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                          precursor
                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 493.5;
Pred. No. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                    A
                                                                                                                                                                                                                                                                                                                                                                                       A
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d protein
                                                                        493; DB 6;
No. 4.3e-30;
                                                                                                                                                         493;
No. 4.
                                                                                                                                                                                                                                        493;
No. 4
                                                                                                                                                                                                                                                                                                                          493;
No. 4
                                                                                                                                                                                                                                                                                                                                                                                                          493; DB 8;
No. 4.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493.5; DB 6
No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494;
No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494;
No. 3.
                                                                                                                                                                                                         designated
                                                                                                                                                                                                                                        4.2e-30;
                                                                                                                                                                                                                                                                                                                         4.2e-30;
                                                                                                                         protein
 ВB
                                                                                                                                                        DB
.3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 3
.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
.6e-30;
 7;
                                                                                                                                                        -30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
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                                                                                                                         SEQ
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Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 262;
                                                                                                                         IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
                                                                                                                         NO:600
                                                                                                                                                                262;
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Ade.
Best
RESULT 1'
ID '
                                                                         Best Local Similarity
RESULT 1270
ID ABG77002 standard; p
DE Human kallikrein 1 p
PN W0200261131-A2.
PD 08-AUG-2002.
PA (BRIM ) BRISTOL-MYER
PA (TSUC/) TSUCHIHASHI
PA (HUIL/) HUI L.
                                          Query Match
Best Local Similarity
RESULT 1271
                                                                                                                                                                                                                                                Best Local Similarity RESULT 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 1263
ID ADM72846 standard; p
DE Human glandular kall
PN W02004022709-A2.
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1265
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                               ABG76998 standard; p
Human kallikrein pro
WO200261131-A2.
08-AUG-2002.
Human NOV18g protein SEQ ID WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-2001.
(UYAR-) UNIV ARKANSAS.
(UYAR-) 35.8%;
Match 35.8%;
                                                                                                                     ABG77002 standard; protein; 262 AA. Human kallikrein 1 polymorphic sequ WO200261131-A2.
                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.

XY Match

15 Local Similarity 40.4%;
                                                                                                                                                                                                             Human pancreatic WO200055320-A1.
                                                                                                                                                                                                                     AAB54293 standard; protein; 267 Human pancreatic cancer antigen
                                                                                                                                                                                                   21-SEP-2000
                                                                                  (BRIM ) BRISTOL-MYERS SQUIBB (TSUC/) TSUCHIHASHI Z.
                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB
(TSUC/) TSUCHIHASHI Z.
(HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-1989.
(AMGE-) AMGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                    Kallikrein encoded EP297913-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP95121 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TRYI trypsinogen variant WO9910503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 35.8%;
Local Similarity 41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) ROCHE DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW93488 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM72846 standard; protein;
Human glandular kallikrein;
WC2004022709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB98503 standard; protein; 225 AA.
Human trypsin serine protease catalytic
WO200129056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MANN-) MANNKIND CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                    i; protein;
protein vai
                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 262 AA.
by clone lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                  35.7%;
                                                                                                                                                                                                                                                       35.8%;
                                                                                                                                                                                                                                                                                                                                                                     35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%;
43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.4%;
                                                                                                                                                                                                                                                                                                                                    in; 262 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GMBH.
3%; Score
7%; Pred.
                224 AA.
NO:104.
                                                 Score
Pred.
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Pred.
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Pred. No. 5.
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Pred.
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Pred.
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Pred.
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protein
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Pred.
                                                                                                                              sequence
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t #2.
                                                                                                                                                                                                                    AA.
protein
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                                                 491;
No. 6.
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No. 5.
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No. 5.
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No. !
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No. 4.
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No. 4
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No. 4.
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5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4e-30;
                                                                                                                                                                                                                    sequence
                                                 DB 5;
.2e-30;
                                                                                                                                                              DB 3;
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.2e-30;
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.2e-30;
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..5e-30;
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.3e-30;
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10-APR-2003

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watch

dest Local Similarity

RESULT 1274

ID AAY25510 stand

DE Human pro-

PN EP936
                                                           RESULT
ID AD
DE An
PN WO
PD 08
                         Best Local Similarity RESULT 1276
                                                                                                                                                                                                                                        Query Match 35.7%;
Best Local Similarity 45.3%;
RESULT 1273
                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1272
                                   Query Match
Best Local
                                                                                                               Query Match
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                                                                   ADN04726 standard; protein; 247 AA. Antipsoriatic protein sequence #544. W02004028479-A2.
                                                                                                                                                  AAY25510 standard; protein; Human prostate serine protes
                                                                                                                                                                                                              Human serine protease, WO200125446-A1.
ADN99593 standard; protein; 2
Novel human protein sequence
WO2004038003-A2.
                                                                                                                                                                                                                              AAE00397 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GUOX/)
(PATT/)
(SPYT/)
(EDIN/)
(ELLE/)
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US2004038223-A1.
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                                                             08-APR-2004.
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                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                    SPAD/)
                                                                                             Local Similarity
                                                                                                                        ) BASF AG.
                                                                                                                                                                                                                                                                ) AGEE M L.
) BERGHS C.
) DIFIPO V A.
) EISEN A.
) GANGOLLI E A.
) RIEGER D K.
) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) SMITHSON G.
) MILLET I.
) PEYMAN J A.
) KEKUDA R.
                                                                                                                                                                                                                                                                                                                              MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                      ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
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                                 35.5%;
42.3%;
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43.9%;
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43.0%;
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45.3%;
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        247 AA.
e #409.
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                                 Score
Pred.
                                                                                                                                                                            Score 489.5; DB 4;
Pred. No. 7.2e-30;
                                                                                                                                                                                                                                                 Score
Pred.
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Pred.
                                                                                                       Score 488.5; DB 2;
Pred. No. 8.4e-30;
                                 No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490; DB 6;
No. 6.3e-30;
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No. 6.3e-30;
                                 9.9e-30;
                                         Length
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                                                                                                               Length 231;
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Query Matc
Best Local
RESULT 1280
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RESULT
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RESULT 1277
ID AAM01227 standard;
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RESULT 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU71763 standard; p
Prostate cancer spec
US2002192763-A1.
19-DEC-2002.
                                                                                                                                                                                                       Human P703P/PSA
US2002022248-A1.
21-FEB-2002.
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P703P and PSA fusic
                                                                                                                                                                       (XUJJ/)
(MITC/)
                                                                                                                                                                                                                            ABB95332 standard; protein;
Human P703P/PSA fusion prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FIVE-) FIVE PRIME THERAPEUTICS INC.
ry Match 35.5%; Score 488;
Liccal Similarity 42.3%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                  (MCNE
 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                               STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                          HURAL J.

MCNEILL P D.

HOUGHTON R L.

Y DE BASSOLS C V
                                                                                                                                                           DILLON D C.
MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                          STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                  JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
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HEPLER W T.
HENDERSON R A.
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KALOS M D.
FANGER G R.
RETTER M W.
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                     HENDERSON R
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35.5%;
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44.1%;
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Score
Pred.
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Pred.
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Pred.
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en fusion
 487.5; DB
No. 2e-29;
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No. 2e-29;
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No. 2e-29;
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No. 2e-29;
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Query Match
Best Local Similarity
RESULT 1285
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Best Local S
RESULT 1283
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Best Local Similarity
RESULT 1282
ID ADB14067 standard;
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                                  (VEDV)
                                                                                                                       US2002192763-A1.
19-DEC-2002
                                                                                                                                             ABU71888 standard; protein;
                                                                                                                                                                                                                   (SKEI/)
(HEPL/)
(HEND/)
                                                                                                                                                                                                     (HURA/)
                                                                                                                                                                                                                                                                                                                                                                ABU71889 standard; protein; Prostate cancer specific ant US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate specific protein US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate-specific US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG26483 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR54444 standard; protein; 449 prostate tumour specific protein W0200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
                                                      DILLON D C.
MITCHAM J L.
HARLOCKER S JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                              STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                 CARTER D.
LI S X.
WANG A.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                            HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                                                                                                                                                  STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                       JIANG Y.

KALOS M D.

FANGER G R.

RETTER M W.
                                                                                                                XU J.
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HARLOCKER S L.
                                                                                                                                                                                                     MCNEILL P D
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DILLON D C.
                                                                                                                                     cancer associated
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44.1%;
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44.1%;
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polypeptide
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| protein
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Pred.
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Pred.
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Pred.
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P703P/PSA
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                                                                                                                                     #72
                                                                                                                                                           487.5; DB 4;
No. 2.6e-29;
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No. 2e-29;
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No. 2e
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-29;
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Query Match
Best Local S
RESULT 1290
ID AAY31160
DE Human try
PN US5948892
PD 07-SEP-19
                 Query Match
Best Local Similarity
RESULT 1291
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Best Local
RESULT 1286
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Best Local Similarity
RESULT 1289
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Best Local Similarity
RESULT 1288
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Best Local Similarity
RESULT 1287
                                                         Human trypsin serine proteas US5948892-A.
ADL15207 standard; protein; Pancreatic kallikrein #3.
                                           07-SEP-1999
(AMGE-) AMGI
                                                                                                                 (DBAS/)
(FOYT/)
                                                                                                                                                                                                                                                                                                                                                                                   Human prostate-specific polypeptide US2003157089-A1.
                                                                                                                                                            (HEPL)
                                                                                                                                                                                                                                                                                                                     ABU71890 standard; protein; 801 AA. Prostate cancer specific antigen fusion protein US2002192763-AI.
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                                                                                                                                                                                                                                                                                                              19-DEC-2002
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(CORI-) CORIXA CORP.
                                                                                                                                            MCNE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        הבאכישטט standard; protein; Prostate tumour-related prot WO200280747->~
                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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(HEND/)
(HURA/)
                                                                                                                                                         CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
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RETTER M W.
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DAY C H.
VEDVICK T S.
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HARLOCKER S
                                                                                             Similarity
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Y DE BASSOLS C V.
                                                                                                                                          MCNEILL P D.
                                                                                                                                                                                                                                                                                           DILLON D C.
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HOUGHTON R L.
Y DE BASSOLS C V
                                                                                                                                                                                                                                                                     JIANG
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HENDERSON R
HURAL J.
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44.1%;
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44.1%;
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44.1%;
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44.1%;
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protein
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                         487; DB 2;
No. 1.1e-29;
                                                                                            487.5;
No. 3.6
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No.
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No. 2.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                 #249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487.5; DB 4;
No. 2.6e-29;
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                                                                    domain.
                                                                                                                                                                                                                                                                                                                                                      7.5; DB 7;
2.6e-29;
                                                                                             , DB 4
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mary March
Best Local Similarity
RESULT 1292
ID ABM83249 stand-
DE Human dia-
PN WO200
                                                       Query Match
Best Local Similarity
RESULT 1299
ID AAY72526 standard; F
DE Human prostase antig
PN W0200104143-A2.
PD 18-JAN-2001.
PA (SMIK) SMITHKLINE E
PA (CORI-) CORIXA CORP.
                                                                                                                                                               RESULT
ID AA
DE Hu
PN WO
PD 05
PA (S
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                    вевt Local Similarity
RESULT 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW57740 standard; protein;
Trypsinogen-like protein,
JP10099080-A.
                                                                                   Human prostase antigen P703PDE5 sequence. WO200104143-A2.
                                                                                                                                                                                                                                                                                AAP70568 standard; protein; 262 Human kallikrein-like substance JP62126980-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM83249 standard; protein; 261 AA. Human diagnostic and therapeutic pprotein W02004023973-A2.
                                                                                                                                                                                                                                                         09-JUN-1987.
(NAKA/) NAKANISHI S.
                                                                                                                                                                                                                                                                                                                                                                           Human KLK-L1 pr
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pancreatic kallikrein #2.
CN1384199-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM83250 standard; protein; 333 A Human diagnostic and therapeutic
 AAU74902 standard; protein; 2
Protein sequence of prostase
                                                                                                                                                                                      Human serine pr
WO200123587-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     AAB21293 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL15206 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REMI-) REMIN HOSPITAL SHENZHEN CITY.

ry Match 35.3%; Score 484.5;
t Local Similarity 40.2%; Pred. No. 1.
                                                                                                                                     AAU01290 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        (REMI-) REMIN HOSPITAL SHENZHEN CITY.
ry Match 35.2%; Score 48
Local Similarity 39.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                             (MOUN ) MOUNT SINAI HOSPITAL.
TY Match 35.1%;
Local Similarity 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-1998.
(SHIS ) SHISEIDO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE CORP.
                                                         SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-MAR-2004
                                                                                                                                                                                                                        Local Similarity
1298
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1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                      ndard; protein;
protein #1.
                                                                                                                                                                                                 protease
                                                                                                                                                                                                             protein;
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42.5%;
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                                   34.8%;
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HETAA37p.
226 AA.
We homologue
                                                                                                                                                                                                                                                                                                                                                                                                  237
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Pred.
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Pred. No. 3
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Pred.
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c pprotein
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                                   477.5; DB 4;
No. 5.8e-29;
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No.
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No. ;
                                                                                                                                         477.5; DB 4
No. 5.5e-29;
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No. 2.1e-29;
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No. 2.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                      483;
                                                                                                                                                                                                                                                                                            hypotensive
                                                                                                                                                                                                                                    L; DB 1;
. 3.6e-29;
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2.7e-
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2.5e-29;
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1.5e-29;
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Best L
RESULT 1
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Best Local Similarity
RESULT 1306
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RESULT 1304
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RESULT 1303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU74933 standard; protein; 226 AA. Amino acid sequence of prostase pro W0200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU74768 standard; protein; 312 AA.
Amino acid sequence of wild-type NS1-p703-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY72522 standard; protein; 312
NS1-P703P-His fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200200708-A2
                   Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                  Human prostate s
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                       ABU71886 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74929 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK) SMITHKLINE BEECHAM BIOLOGICALS (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                          ABM82601 standard;
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HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                DILLON D C.
MITCHAM J L.
HARLOCKER S !
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                           SMITHKLINE BEECHAM BIOLOGICALS ih 34.8%; Score 477 . Similarity 43.8%; Pred. No.
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th 34.8%;
Similarity 43.8%;
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                                                                                              HOUGHTON R L.
Y DE BASSOLS C V.
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MCNEILL P D.
INCYTE CORP
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specific anti
                              d; protein; 239 F
and therapeutic
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e of wild-type NS1-P703P-His
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43.8%;
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b; Score 477.
b; Pred. No.
                                          239
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                                                               Score 477.5; DB 4;
Pred. No. 8.9e-29;
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                              pprotein
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8.1e-29;
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5.8e-29;
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                                SEQ
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RESULT
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PD 12
PA (C)
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Best Local Similarity
RESULT 1311
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RESULT 1310
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Best Local S
RESULT 1307
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RESULT 1309
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                                AAG62147 standard; protein; Human P703P inventive antigo W0200125273-A2.
                                                                                                             AAG99008 standard; protein;
Human prostate-specific amir
WO200134802-A2.
                                                                                                                                                                                            Prostate tumour antigen predicted WO200125272-A2.
                                                                                                                                                                                                             AAB74806 standard; protein;
                                                                                                                                                                                                                                                                        AAU69768 standard; |
Human prostate cDNA
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                       AAM01123 standard; protein; 220 AA Human prostate-specific amino acid W0200151633-A2.
                                                                                                      17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200004149-A2.
                                                                                          CORI-) CORIXA CORP.
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(FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human diagnostic and therapa

MOMONA 23973-A2.
                                                               Local Similarity
1315
                                                                                                                                                                                    .2-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY82008 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN99649 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM82603 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2852.
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                                                                                                                                                                                                                                 Local Similarity
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            CORIXA CORP.
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                                                                                                                                                                                                                                                                                   protein;
A encoded
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prostate tumour protein
                                                                     34.4%;
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  34.4%;
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                                       otein; 220 AA.
antigen SEQ ID
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40.1%;
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Protein
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e #465.
   Score
                                                                    Score 472.5; DB 4;
Pred. No. 1.4e-28;
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No. 1.4
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No. 1.4e-28;
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No.
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No. 8.8e-29;
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No. 8.8e-29;
                                        NO:
                                                                                                                                                                                                                                                                                 #8
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. 1.4e-28;
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1.4e-28;
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                                        330.
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.6e-28;
  В
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BBBB

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DE P...ery Match CORP Best Local Similarity RESULT 1320
                                                                                                                              Query Match
Best Local Similarity
RESULT 1318
ID ABR54340 standard; pro
DE Prostate tumour specif
PN W0200289747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
                                                           Best Local Similarity
RESULT 1319
ID ADB13777 standard; p
DE Human prostate speci
PN US2003185830-A1.
PD 02-OCT-2003.
                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1316
                                                             Human prostate specific prot
US2003185830-A1.
                                             02-OCT-2003.
(CORI-) CORIXA CORP
ADG26193 standard; protein; 220 AA. Human prostate-specific polypeptide
                                                                                                                                                        ABRS4340 standard; protein; 220
Prostate tumour specific protein
                                                                                                                                                                                                                                                                                                                                                                                         US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                 ABB95228 standard; protein;
Human P703PDE5 protein SEQ
                                                                                                                                                                                                              (HEND/)
                                                                                                                                                                                                                                SKEI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU71659 standard; protein; Prostate cancer specific ant
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LI S X.
WANG A.
SKEIKY Y A W
HEPLER W T.
HENDERSON R
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MITCHAM J L.

HARLOCKER S 1
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FANGER G R.
RETTER M W.
STOLK J A.
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) HEPLER W T.
HENDERSON R A.
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VEDVICK T S
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DAY C H.
VEDVICK T S.
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KALOS M D.
FANGER G R.
RETTER M W.
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MITCHAM J L.
HARLOCKER S I
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Y DE BASSOLS C
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protein
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                                                                                                                                                          protein sequence
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antigen P703P
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ID NO 327.
                                                                                                         Score
Pred.
                            Score 472.5; DB 7
Pred. No. 1.4e-28;
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Pred.
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P703PDE5
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                                                                                                       472.5; DB 6
No. 1.4e-28;
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No. 1.4e-28;
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Best Local Similarity

RESULT 1328

ID AAY56048 stand

DE Human pro-

PN W099-
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RESULT 1321
ID ADI39732 standard; p
DE Human glandular kall
PN US6642013-B1.
PD 04-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1322
ID ADI3715
DE Human g
PN US20031
PD 23-OCT-
Query Match 34.2%;
Best Local Similarity 40.4%;
RESULT 1329
ID AAY77842 standard; protein;
DE Human prostate-specific anti
PN WO9960984-A2.
                                                                                                                                                                                                                                                                                               pest Local Similarity
RESULT 1326
                                                                                                                                                                                                           RESULT 1327
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                                                                                                                                                                          AAW13649 standard; protein; Human prostatic specific ant W09711172-A1.
                                                                                                                                                                                                                                                                  AAU06276 standard;
Prostate specific !
WO200145728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR96163 standard; protein;
Human NOV12a protein SEQ ID
WO200290568-A2.
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Human glandular kallikrein
US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP92314 standard; protein;
Human recombiant kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI39732 standard; protein; 262 AA.
Human glandular kallikrein (Hk2) protein.
US6642013-B1.
                                                                                                AAY56048 standard; protein; 261 AA.
Human prostate-specific antigen.
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(AMGE-) AMGEN.
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                                                                                                                                                                                                                                                                                                                                                                               AAB21313 standard;
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21-AUG-2003.
                                                                 (UYPE-) UNIV
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34.2%;
ilarity 40.4%;
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34.2%; Score 470.
y 40.4%; Pred. No.
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34.2%;
40.4%;
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           antigen
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antigen.
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(hHk2)
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NO:68.
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(PSA)
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No.
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No.
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No. 1.6e-28;
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No. 2e-28;
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No. 1.7e-28;
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No. 2.3e-28;
                                                                                                                                 .5; DB 2;
2.3e-28;
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1.6e-28;
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1.4e-28;
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2.3e-28;
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2.3e-28;
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Best Local Similarity RESULT 1335
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RESULT 1334
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RESULT 1332
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Best Local Similarity
RESULT 1330
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  Best Local Similarity
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14-SEP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
(MOUN ) 34-2%;
ery Match 34-2%;
                                                                                                                                                                                                                                                                                                                                                                                       Human prostate specific anti WO200125273-A2.
                                      Human PSA protein WO200281646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB74821 standard; protein; 261 AA. Prostate tumour antigen amino acid W0200125272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG62144 standard; protein; Human prostate specific meml WO200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PSA.
WO200053776-A2
                                                         ABP74202 standard;
                                                                                                                                                                                                                                                                                                           Human prostatic
US2002192763-A1.
19-DEC-2002.
                                                                                                                                                                                                                                                                                                                                       ABU71859 standard; protein;
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SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
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HARLOCKER S
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DAY C H.
VEDVICK T S.
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KALOS M D.
FANGER G R.
RETTER M W.
CTL IMMUNOTHERAPIES h 34.2%; Similarity 40.4%;
                                                                                              FOY
                                                                                                      HOUGHTON R L.
Y DE BASSOLS C
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                                               ; protein; SEQ ID NO:
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                                                                           34.2%;
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antigen
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No. 2.3e-28;
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No. 2.3e-28;
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No. 2.3e-28;
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No. 2.3e-28;
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No. 2.3e-28;
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2.3e-28;
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RESULT 1341
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Best L
RESULT 1
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RESULT
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ID ADB82777 standard;
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    Best
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                                                                                                                                                                                                                                                                                                                        US20003.
23-007-2003.
(UYAR-) UNIV ARKANSAS.
(UYAR-) 34.2%; (34.2%; (40.4%;
                                                 AAG62154 standard; protein; 6
Human WT1/PSA fusion protein
                                Human WT1/PSA fusion WO200125273-A2. 12-APR-2001.
                                                                                                                        AAB08449 standard; protein; 375 AP A human prostate specific antigen WO200049158-A2.
                                                                                                                                                                                                                                                                                                                                                            Human prostate specific antigen US2003199010-A1.
                                                                                                                                                                                                Tumour-associated WO2004030615-A2. 15-APR-2004.
                                                                                                                                                                                                                 ABM82166 standard; protein; Tumour-associated antigenic
                                                                                                                                                                                                                                                                                     Human PSA protein SEQ ID NO:78. WC2004 022709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH) US DEPT HEALTH & HUMAN SERVICES.
Fig Match 34.2%; Score 470.5; DB 7
St Local Similarity 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                    (MANN-) MANNKIND CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate US6642013-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence useful for the WO2003050236-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-2003
(UYAR-) UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI39733 standard; protein; 261
Human prostate specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC09580 standard;
PSA protein #SEQ II
WO2003008537-A2.
                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PSA precursor WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ59022 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003.
(CTLI-) CTL IMMUNOTHERAPIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L2-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Match
  Similarity
                                                                                                    COMPUGEN LTD.
                                                                                                                                                                                      GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV ARKANSAS MEDICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
D 78.
 34.2%;
                                                                                34.2%;
                                                                                                                                                                34.2%;
                                                                                                                                                                                                                                                 34.2%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%;
                                                  692 AA.
n SEQ ID
                                                                                                                                                                                                                  261 AA.
target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 AA. sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP.
Score 470.5; DB 7
Pred. No. 2.3e-28;
                                                                                Score
Pred.
Score 470.5; DB 4;
Pred. No. 6.3e-28;
                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 470.5;
Pred. No. 2.
                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                   AA.
(hPSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
(PSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                 variant
                                                                               470.
No.
                                                                                                                                                                470
No.
                                                                                                                                                                                                                                                470.5; DB 8
No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                470.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                470.
No.
                                                                                                                                                                                                                  (TAT)
                                                   ŏ:
                                                                              3.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                .5; DB 8;
2.3e-28;
                                                                                                                                                                                                                                                                                                                                2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cancer (SeqID 1558).
                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 8;
                                                                                                                                                                                                                 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 7
.3e-28;
                                                                                                                               polypeptide
                                                                                         ω
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8
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        Length
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                                                                                                                                                                                                                PRO2109,
                                                                                         375;
                                                                                                                                                                          261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261;
                                                                                                                                                                                                                SEQ:5591
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wery Match
Best Local Similarity
RESULT 1333
ID AAR82703 stap*
PN JP077
                                                                                                                                         Best Local Similarity
RESULT 1352
ID AAP81243 standard; p
DE Human spleen trypsin
PN JP63160582-A.
PD 04-JUL-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1345
ID AAB67545 standard; p
DE Amino acid sequence
PN w0200116289-A2.
PD 08-MAR-2001.
                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1351
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
RESULT 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
RESULT 1347
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                               AAU74767 standard; pi
Amino acid sequence o
WO200200708-A2.
03-JAN-2002.
                                                   AAR82703 standard; protein; 2 Human pancreatic trypsin III. JP07184655-A.
                                                                                                                                               Human spleen trypsin III (trysinogen UP63160582-A.
                                                                                                                                                                                                                                                       AAU74928 standard; p
Amino acid sequence
WO200200867-A1.
                                                                                                                                                                                                                                                                                                      03-JAN-2002.
03-JAN-2002.
(SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
34.0%; Score 467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY72521 standard; protein; 312
NS1-P703P mutated-His fusion pro
WO200104143-A2.
18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU74934 standard; protein; 231 AA.
Amino acid sequence of P703P mutated-His
WC200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74903 standard; p
Amino acid sequence
WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PSA precursor WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.

TY Match 34.1%; Score 468.5

Local Similarity 40.4%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ59024 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ORTH
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORTHO-MCNEIL PHARM tch 34.1%; al Similarity 43.8%;
                          SANKYO CO LTD.
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHKLINE
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                                                                                                                            LTD.
                                                                                                                                                                                                     BEECHAM BIOLOGICALS.
34.0%; Score 467.
43.4%; Pred. No.
                                                                                                                                                                                                                                                                    protein; 312 AA
e of NS1-P703P mu
                                                                                                                                                                                                                                                                                                                                                                    protein; 312 AA.
e of NS1-p703 mutated-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
e of p703
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34.0%; Score 467.
43.4%; Pred. No.
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e of protease
 34.0%;
                                                                                                   34.0%;
40.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                            34.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W INC.

k; Score 469; 1

k; Pred. No. 3.
                                                                           247
 Score
Pred.
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Pred.
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mutated-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA.
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           Score 467.5; DB 4
Pred. No. 4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 467.5;
Pred. No. 3.
                                                                           Å
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MH2 catalytic domain in
                                                                                                                                                                                                                                                                    mutated-His
467; DB
No. 4.1e-
                                                                                                   467; DB 1;
No. 4.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468.5; DB 7;
No. 3.3e-28;
                                                                                                                                                                                                                                                                                                       7.5; DB 5;
. 4.8e-28;
                                                                                                                                                                                                      4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5; DB 5;
3.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion
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.3e-28;
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 28.
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                                                                                                                                                                                                                                                                    fusion
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          Length
                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 312;
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                                                                                                                                                                                                                                                                   protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231;
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JOSENT.

J HERMANN.

A) PILARSKY C

J Match

Local Similarity

JEL Local Similarity

JEL Local Similarity

LSULT 1361

ID ADR66934 standar<sup>2</sup>

DE Human prostat<sup>4</sup>

PN W020040766<sup>3</sup>

PD 10-SEP-<sup>2</sup>

PA (HIN<sup>7</sup>

PA (FIN<sup>7</sup>

P
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ID ADR6627

DE Human p
PN WO20040
PD 10-SEP-
PA (HINZ/)
PA (DAHL/)
PA (ROSE/)
PA (ROSE/)
PA (FILA/)
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ID ALL
DE HU
PN WC
PD 10C
PD (E
PA (E
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RESULT 1356
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RESULT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1354
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR66838 standard; protein; Human prostatic carcinoma de WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM12395 standard; protein; 261 AA.
Human prostate-specific antigen protein.
US2003235594-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB84422 standard; peptide; Rat SCCE protein N-terminal WO200262135-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR66277 standard; protein; Human prostatic carcinoma de WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ59026 standard; protein; 261 AA.
Human PSA analogue (Y154) precursor protein sequence.
                                                                                                                                 ADR66934 standard; protein; Human prostatic carcinoma de WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ANTI-) ANTIGEN EXPRESS INC.
ry Match 33.7%;
Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA50549 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PSA analogue
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ59028 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.

TY Match 33.8%; Score 464.5; DB 7
Local Similarity 40.4%; Pred. No. 6.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
TY Match 34.0%; Score 466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGEL/) EGELRUD T.
HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       /) HINZMANN B.
/) DAHL E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ard; protein; 237 AA.
prostate specific antigen (PSA/KLK3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 261 AA. (L155/Y154) precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.0%;
                                                                                                                                                                                                                                                      33.7%;
40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.7%;
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42.6%;
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42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; 248 AA.
derived p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; 248 AA.
derived D
                                                                                                                                                                derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AA.
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Pred.
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Pred.
                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 462.5; DB 8; Pred. No. 9.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
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                                                                                                                                                                DNA
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No.
                                                                                                                                                                                                                                                   462.5; DB 8;
No. 9.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463.5; DB 8
No. 8.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464; DB 6;
No. 6.7e-28;
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No. 4.7e-28;
                                                                                                                                                                SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.5; DB 5;
. 5.8e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261;
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Best Local Similarity RESULT 1369
                                                                                                                                               Query Match
Best Local Similarity
RESULT 1368
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RESULT 1367
                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
RESULT 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1365
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RESULT 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1363
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Best Local Similarity
RESULT 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Human KLK2.
WO200053776-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                      Human prepro-Trp226-glandular kallikrein-2.
W09701630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2004.
(EXON-) EXONHIT THERAPEUTICS 33.6%;
EXY Match 33.6%;
41.0%;
                                                                                                                                                                                                                                             AAU98921 standard; protein; 245 Human prostate specific antigen WO200240059-A2.
                                                                                                                      AAY08894 standard; protein; 238 AA. Chimeric serine protease FXT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR84668 standard; protein;
Prepro-hK2 kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP27546 standard;
Human kallikrein-3
                                 AAB21314 standard;
                                                                                   07-JUL-1999
(HOFF ) ROC
                                                                                                          EP927764-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP27545 standard;
Human kallikrein-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2848569-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostatic
                                                                                                                                                                                 (AMBI-) AMERICAN FOUND (MINC/) MINCHEFF M S. (LOUK/) LOUKINOV D I. (ZOUB/) ZOUBAK S.
                                                                                                                                                                                                                                                                                                                                   16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                      (MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EXON-) EXONHIT THERAPEUTICS ry Match 33.6%; Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR66036 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HERM/) HERMANN K.
                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L/) DAHL E.
E/) ROSENTHAL A.
M/) HERMANN K.
                                               ROCHE DIAGNOSTICS GMBH.

33.4%; Score 459; DB 2;

3.4%; pred. No. 1.6e-27;
                                                                                                                                                                                                                                                                                                                      ORION YHTYMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILARSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; (KLK-3) E
                                 protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 297 AA. (KLK-3) EHT103 p
                                                                                                                                                                                                                                                                                            AE OY.
33.5%;
40.2%;
                                                                                                                                                          33.4%;
                                                                                                                                                                                                                                                                                                                                                                                              33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.7%;
40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.7%;
                                                                                                                                                                                                                        BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 281 AA.
EHT103 protien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SA.
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SA.
Score 462; DB 8;
Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                              Score 460.5; DB 2; Pred. No. 1.4e-27;
                                                                                                                                                          Score 459.5; DB 5;
Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 462.5; DB 8; Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 462.5; DB 8; Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                        AA.
(PSA) variant.
                                                                                                                                                                                                                        RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protien
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                                                                                                                                                                                                                                                                                               460.5; DB 2;
No. 1.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462; DB 8;
No. 1.1e-27;
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                                                                                                                                                                                                                                                                                                            261;
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Best Local Similarity
RESULT 1377
                                                                                                    PAPA
                                                                                                                                                      Best Local Similarity RESULT 1376
                                                                                                                                                                                                                                       Best Local Similarity RESULT 1375
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Best Local Similarity
RESULT 1374
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Best Local S
RESULT 1373
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RESULT 1370
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                          AAW45397 standard; protein; 26
Prostate-specific glandular ka
W09802748-Al.
22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
133.4%; 1
1881 Local Similarity 40.8%; 1
                                ADB75390 standard; protein; 261
Prostate cancer marker protein.
WO2003009814-A2.
                                                                                                                    AAU06279 standard; protein; 261 AA.
Human Kallikrein2 polypeptide.
WO200145728-A2.
                                                                                                                                                                                                       Human KLK2.
WO200053776-A2.
                                                                                                                                                                                                                         AAB21318 standard;
                                                                                                                                                                                                                                                                                                            AAW96189 standard; protein; Prepro human Kallikrein 2 (p WO9859073-A1.
                                                                                                                                                                                                                                                                (MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                              EPIM-) EPIMMUNE INC.
                                                                                                                                                                                 (MOUN ) MOUNT SINAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW49085 standard; protein; Wild-type human Kallikrein 2 W09821365-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BAYU) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION 50:17 Match 33.4%; Scott Local Similarity 40.8%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW83203 standard; protein;
Prostate-specific glandular
W09846795-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW06971 standard; protein;
Prostate-specific glandular
W09634964-A2.
07-NOV-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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  MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUNT SINAI
                                                                                                                                                                                                                         protein;
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                                                                          33.4%;
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                                                                                                                                                                                 HOSPITAL.
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                                                                                                                                                                                                                                                                                                                               n; 261 AA.
(preprohK2)
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2 (hK2).
                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA.
kallikrein precursor
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kallikrein
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kallikrein p
   Score
                                                                         Score 458.5;
Pred. No. 2e-
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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   458.5;
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No.
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No.
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No. 2e
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No. 2e-27;
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No. 2e-27;
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No. 2e-
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No. 1.9
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2e-27;
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                                                                                                                                                           DB
-27;
                                                                         DB
-27;
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.9e-27;
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-27;
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Length
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Best Local Similarity
RESULT 1384
ID ADA50546 standard; p:
DE Human prostate specif
PN w02003031569-A2.
PD 17-APR-2003.
                                                                                                Best Local Similarity RESULT 1385
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1382
                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1381
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Best Local Similarity
RESULT 1380
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RESULT 1378
              Query Match
                                                                                                                      Query Match
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                                                   Human mature prostate specific a US2003059864-A1.
                                                                                                                                                          ADA50546 standard; protein; 237 Human prostate specific antigen W02003031569-A2.
                                                                                                                                                                                                                                                           AAB19818 standard; protein; 237 AA. Prostate specific antigen elevated WO200066718-A1.
                                                                                                                                                                                                                                                                                                                                                                                AAB19819 standard; protein; 237 AA Prostate specific antigen specific WO200067030-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate-specific antigen EP1043394-A2.
11-OCT-2000.
                         (MIKO/) MIKOLAJCZYK (RITT/) RITTENHOUSE
                                                                                                                                                                                                                                                                                                                                           (HYBR-) HYBRITECH INC.
(BAYU) BAYLOR COLLEGE MEDICINE.
                                                                                                                                  (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                    (HYBR-)
(BAYU )
                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000
(HYBR-) HYBI
                                                                                                                                                                                                                                                                                                                                                                                                                           (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.

"YY Match
33.3%; Score 457.5; DB 3;

t Local Similarity 41.6%; Pred. No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate specific anti W09810292-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96187 standard; protein;
Human prostate specific anti
WO9859073-A1.
30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1998.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9846795-A1.
22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW83213 standard;
Prostate-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                      HYBRITECH INC.
BAYLOR COLLEGE MEDICINE.
h 33.3%; Score
Similarity 41.6%; Pred.
 Similarity
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antigen pr
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 33.3%;
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41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ein; 237
antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 AA.
igen N-terminal
Score
Pred.
                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 457.5; DB 2;
Pred. No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                      antigen
                                                                                                                                                                   AA.
(PSA/KLK3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PSA).
457.5; DB 6
No. 2.1e-27;
                                                                                                         457.5; DB 6;
No. 2.1e-27;
                                                                                                                                                                                                          457.5; DB 4;
No. 2.1e-27;
                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                    457.5; DB 4;
No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÞΚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457.5; DB 2;
No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457.5; DB 2
No. 2.1e-27;
                                                                                                                                                                                                                                                                             benign
                                                                                                                                                                                                                                                                                                                                                                                        benign
                                                                      (PSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment
                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                              prostatic hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                         prostatic hyperplasia.
          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                      ij
         Length
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                                                                                                                                                                     NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
           237;
                                                                                                                                                                                                                   237;
                                                                                                                    237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237;
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RESULT
ID AA
DE HO
PN WO
PD 26
                                                                                                                                                                                                                                                                                 RESULT 1391
ID AAW069
DE Kallik
PN WO9634
PD 07-NOV
PA (HYBR-
PA (MAYO-
                                                                                                                                                                                                                                            Dest Local Similarity
RESULT 1392
Query Match 33.1%; Score
Best Local Similarity 43.8%; Pred.
RESULT 1394

ID AAY72523 standard; protein; 232 AA.
DE Human prostase antigen #1.
PN W0200104143-A2.
PD 18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1388
                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                             Query
                                                                                                                                                                                                          AAW45400 standard;
Prostate-specific of WO9802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate specific antigen US2003166036-A1.
                                                                                                                                                                                                                                                                                                                   AAW06972 standard; protein; 261 AA. Kallikrein prepro-hK2v217 variant. W09634964-A2.
                                                                                                   AAW59129 standard; protein;
Homo sapiens Tub Interactor
WO9812302-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               Human PSA mature WO2003047506-A2.
                                                    (MILL-) MILLENNIUM PHARM INC.
ry Match 33.1%;
t Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ59025 standard; protein;
Human PSA mature protein sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW45398 standard; protein;
Prostate-specific antigen pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kallikrein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70677 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MIKO/) MIKOLAJCZYK S D.
(RITT/) RITTENHOUSE H G.
ry Match 33.3%;
t Local Similarity 41.6%;
                                                                                                                                                                        (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOT-) BIOTECHN RES PARTN.
(CALB-) CALIF BIOTECHNOL INC.
ry Match 33.2%;
Local Similarity 39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PSA mature
                                                                                                                                                                                                                                                                                 (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.

ry Match
33.3%; Score 457.5; DB 7
Local Similarity
41.6%; Pred. No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                         US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                      l; protein;
glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 24
ene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                 33.2%;
                                                                                                                                                 33.2%;
                                                                                                                                                                                                                                                          33.2%;
40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n; 237 AA.
protein h
                                                                                                                                                                                                                                                                                                                                                                                                                                   237 AA.
                                                                                                                232 AA.
(hTI-1)
                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
                                                                                                                                                                                                                      261 AA.
kallikrein hK2v217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 AA
                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 457.
Pred. No.
                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 456; DB 1;
Pred. No. 2.9e-27;
                                                                                                                                                                                                                                                          Score 455.5; DB 2; Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
(PSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   አሪ
                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                   455
No.
                                                       454.
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              455.
No.
                                                                                                                protein
                                                                                                                                                   5.5; DB 2;
. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5; DB
3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5; DB 8;
2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                  .5; DB 7;
3e-27;
                                                        .5; DB 2;
3.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 237;
                                                                                                                                                             Length
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                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                              237;
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Best Local
RESULT 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
RESULT 1399
                                                                                                                  Best Loca
RESULT 1402
                                                                                                                                                                                                                                      Best Local Similarity RESULT 1401
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
RESULT 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1397
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                        (MAYO-) MAYO FOUNDATION.
(MYBR-) HYBRITECH INC.
(HYBR-) 32.9%;
uery Match
32.9%;
41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O3-JAN-2002.
O3-JAN-2002.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
EXP Match
33.1% Score 454.
**Coal Similarity 43.8% Pred. No.
                                                                                                                                                                                                                                                                                                      Prostate-specific WO9846795-A1. 22-OCT-1998.
                                                                                                                                                                                                         AAW45396 standard; protein;
Prostate-specific glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ59027 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO38617 standard; protein; 261 AA.
Prostate Specific Antigen (PSA).
US200405881-A1.
25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR84669 standard; protein;
Pro-hK2 kallikrein.
WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74930 standard; protein; 232 AA. Amino acid sequence of prostase protein w0200200867-A1.
                                                                                       AAW96188 standard, protein; 244
Pro human Kallikrein 2 (prohK2).
                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                           AAW83204 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human PSA analogue
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ANTI-) ANTIGEN EXPRESS INC.
ry Match 33.1%;
t Local Similarity 39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74769 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
         MAYO FOUNDATION.
YOUNG C Y F.
TINDALL D J.
KLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITHKLINE BEECHAM BIOLOGICALS.

th 33.1%; Score 454.5;
Similarity 43.8%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                     DEPT HEALTH & HUMAN SERVICES
33.0%; Score 453.1
milarity 41.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                               ; protein;
glandular
                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 237 AA. (Y154) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 232 AA.
prostase homologue
                                                                                                                                                                                                                                                   32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.1%;
32.9%;
                                                                                                                                                                                                           244 AA.
kallikrein
                                                                                                                                                                                                                                                                                                                                244 AA.
kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AA
                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                   Score
Pred.
Score 452.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 454.5; DB Pred. No. 4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 454.5; DB 5; Pred. No. 3.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 454.5; DB 4;
Pred. No. 3.5e-27;
                                                                                                                               452
No.
                                                                                                                                                                                                                                                   452
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454
No.
                                                                                                                                                                                                                                                   2.5; DB 2;
5.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5; DB 2;
3.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5; DB 5;
. 3.5e-27;
                                                                                                                               5.3e-27;
                                                                                                                                                                                                                                                                                                                                                                       .5; DB 7;
4.3e-27;
                                                                                                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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2
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Length
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                                                                                                                                                                                                                                                                  244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232;
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Adery M.
Best Loca.
RESULT 1409
ID AAW457
DE Mat'
PN W'
PD PD
PD
                        Best Local Similarity
RESULT 1411
                                                                        PA
PA
PA
PA
PA
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Best Local Similarity
RESULT 1408
                                                                                                                                                        RESULT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1404
                                                 Query Match
                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA50561 standard; protein; 237 AA. Kallikrein KLK2, SEQ ID NO:16.
                                                                                                                 AAW96186 standard; protein;
Mature human Kallikrein 2 ()
WO9859073-A1.
                                                                                                                                                                                                                                                                                                                          Prostate-specific glandular kallikrein WO9846795-Al.
                                                                                                                                                                                                                          AAW45395 standard; protein; 237 AA.
Mature prostate-specific glandular kallikrein hK2
W09802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAR77098 standard; protein; 237 AA. Prostate-specific antigen. W09528498-A1. 26-OCT-1995.
                                                        (MAYO-) MAYO FOUNDATION
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                                  22-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2004.

18-JUN-2004.

(EXON-) EXONHIT THERAPEUTICS SA.

18-JUN-2004.

32.9%; Score

19-Jun-2004.

32.9%; Score

19-Jun-2004.

32.9%; Pred.
                                                                                                                                                                                       (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                         (UYCO) UNIV COLUMBIA NEW YORK.
ry Match 32.8%; Score
t Local Similarity 40.7%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP27537 standard;
Human kallikrein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP27538 standard;
Human kallikrein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW03130 standard;
Prostate-specific a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ59029 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EXON-) EXONHIT THERAPEUTICS TY MATCH 32.9%; Local Similarity 41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9621042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L1-JUL-1996.
(UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 297 AA. (KLK-2) EHT102 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 236 AA. (L155/Y154) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 281 AA. (KLK-2) EHT102 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                   32.8%;
42.0%;
                                                                                                                                                                 32.8%;
42.0%;
                                                                                                                                                                                                                                                                       32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 88 ;
                                                                                                                               n; 237 AA.
(hK2).
                                   Score
Pred.
                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SA.
Score
Pred.
                                                                                                                                                               Score 450.5; DB 2;
Pred. No. 7.4e-27;
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Pred.
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                                   450.5; DB 2;
No. 7.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                            450.
No.
                                                                                                                                                                                                                                                                       450.5; DB 2;
No. 7.4e-27;
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No.
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No.
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No. 5.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
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. 6.5e-27;
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6.1e-27;
                                                                                                                                                                                                                                                                                                                                                                             7.5
                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                            ; DB 2;
.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a variant
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                                             237;
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Query Match
Best Local Similarity
RESULT 1412
ID AAR84667 standard; p
Best Local
RESULT 1417
                                                                                                    Query Match
Best Local Similarity
RESULT 1416
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RESULT 1414
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RESULT 1413
               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                        AAW83212 standard;
hK2 variant A217V.
                     (BAYU ) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
                                               WO9846795-A1.
                                                                                                   (YTIMS)
                                                                                                                    (SCIO/)
                                                                                                                                                                                                                                                                                                                                ADJ83076 standard; protein; 217 / Trypsin protein which is related US2003170630-Al;
                                                                                                                                    (MILL
                                                                                                                                                     (RIEG/
                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide hom WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                           ADI17269 standard; protein; Polypeptide homologous to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI17277 standard; protein; Polypeptide homologous to a WO200268649-A2. 06-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR84667 standard; protein;
Mature kallikrein hK2.
W09530758-A1.
                                                                                                           (MACD/)
                                                                                                                                                                                                                                                                                         (SPYT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2003.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003031569-A2
                                                                                                                                                                                                        CASM/
                                                                                                                                                                                                                                                                                                          TCHE/)
                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                 MACDOUGALL C
                                                                                                                           PERNANDES E R.
RIEGER D K.
EDINGER S R.
GUNTHER E.
MILLET I.
SCIORE P.
                                                                                                                                                                            CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
                                                                                                                                                                                                                   SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURAGEN CORP.
                                                                                                                                                                                                                                                                                                 LIU X.
                                                                                                                                                                                                                                                                                                          TCHERNEV V T.
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                                                                                                          4
                                                               protein;
   32.6%;
                                                                                32.6%;
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                                                                237
    Score 447.5; DB 2;
Pred. No. 1.3e-26;
                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                            human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA
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human N
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Pred.
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Pred.
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Pred.
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Pred. No. 7.
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                                                                                447.5; DB 7;
No. 1.1e-26;
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No.
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No. 1e-26;
                                                                                                                                                                                                                                                                                                                                         human
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.1e-26;
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1.4e-27;
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e-26;
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             Length 237;
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вевt Local Similarity
RESULT 1424
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RESULT 1419
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                     RESULT 1425
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Best Local
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                                                                                                                                                                        AAR94526 standard; protein; Korean Viper Salmosa thromb: EP707067-A2.
                                                                                                                                                                                                                                                                                                                                                           ABM82643 standard; protein; 227 A Human diagnostic and therapeutic WO2004023973-A2.
                                                                                             AAG79000 standard; protein; Mamushi fibrinolytic enzyme,
                                                                                                                                                                                                                                                                       AAR84670 standard; protein;
Mature kallikrein hK2.
WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW96190 standard; protein;
Variant human Kallikrein 2
WO9859073-Al.
AAM52944 standard; protein; 260 AA.
Agkistrodon halys brevicaudus thrombin-likle protease, salmobin.
                                                                                   KR2001045716-A.
                                                                                                                           7-APR-1996.
(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
32.0%; Score 43
CY Match 37.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR84671 standard; protein;
Mature kallikrein hK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM.
ry Match 32.4%;
t Local Similarity 41.0%;
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Human prostate specific antigen.
WO9640754-A1.
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Mutant human Kallikrein 2 (hK2)
                                                     (LEEJ/) LEE J W.
(PARK/) PARK W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                      HYBR-) HYBRITECH
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                                                                                                                                                                                                                                                   MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                      INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                 Local Similarity
                              ocal Similarity
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32.1%;
y 40.9%;
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                               31.8%;
37.9%;
                                                                                                enzyme,
                                                                                                                                                                                  cotein; 279 AA.
thrombin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (hK2).
                                                                                                                                                                                                                                                                                             238
                                                                                              233 AA.
brevinase
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Pred.
                               Score
Pred.
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Pred. No. 3.6e-26;
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Pred.
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Pred.
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Pred.
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Pred.
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A217V
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No. 6
                               436.5;
No. 8.7
                                                                                                                                                                                                                                                                                                                 443;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445;
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No. 1.3e-26;
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No. 1.3e-26;
                                                                                                                                                                                  protease, Halybin
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No. 2.1e-26;
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                               ; DB 4;
.7e-26;
                                                                                                                              DB 2;
.7e-26;
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,7e-
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e-26;
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Query Match
Best Local Similarity
RESULT 1426
ID ABECT
                       Best Local
RESULT 1434
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Best Local Similarity
RESULT 1431
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Best Local Similarity
RESULT 1430
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                                                                                                                     Best Local Similarity
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                                                                                                                                                                            AAM01120 standard; protein; 205 AA. Human prostate-specific amino acid W0200151633-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE78966 standard; protein; Human protein modification a WO2003063688-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1998.
30-MAR-1998.
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
31.7%; Score 436;
31.7%; Pred. No. 1.
                                                                                                                                                                                                                                                                            Human prostate tumour US2002090372-A1.
                                                                                                                                                                                                                                                                                                                                                                                     AAY82005 standard;
Human immunogenic I
WC200004149-A2.
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Protein encoded by prostate
WO9837093-A2.
27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW69388 standard; protein; 205 AA. Prostate tumour specific gene clone DE13 W09837418-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC.
ITY Match 31.3%;
It Local Similarity 39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate WO200071711-A2.
                                                                                  Human prostate cDNA
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB50447 standard; protein; 205 AA.
Human prostate cancer-related intracellular
AAB74803 standard; protein; 205 AA
Prostate tumour antigen predicted (
                                                                                                           AAU69766 standard;
                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1998.
(CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                      (XUJJ/) XU J.
                                                                                                                                                                                                                                                                                                               ABG94414 standard;
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                                    local Similarity
                                                           CORIXA CORP.
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A encoded
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43.7%;
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43.7%;
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43.7%;
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43.7%;
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44.2%;
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and m
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protein
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tumour
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Pred.
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Pred.
                                    Score 426.5; DB 4;
Pred. No. 4.5e-25;
                                                                                                                                 Score 426.5; DB 4; Pred. No. 4.5e-25;
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Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                   05 AA.
partial variant
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maintenance molecule
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 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430;
No. 2.
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No.
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No.
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                                                                                                                                                                                                                              426.5; DB 3;
No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone
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No. 4.5e-25;
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1.8e-25;
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.1e-25;
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.7e-25;
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  for P703P-DE13.
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                                                                                                                                                                                                                                                                                                     #2
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RESULT 1438
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DE CONTROL
DE CONTR
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Best Local Similarity
RESULT 1436
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RESULT 1435
          Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                         ABB95225 standard; protein;
Human P703P-DE13 protein SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate tumour US6262245-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU04964 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate-specific amin W0200134802-A2.
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12-APR-2001.
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Prostate cancer specific ant
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          Match
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') FOY T M.
ch
                                                                                                                                                                                                                                                                         ) XU J.
) DILLON D C.
) MITCHAM J L.
) HARLOCKER S I
                                                                                                                     KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
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HEPLEK .. .
HENDERSON R A.
31.0%;
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HEPLER W T.
HENDERSON R A.
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RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
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MITCHAM J L.
HARLOCKER S L.
                                                HEPLER W T.
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LI S X.
WANG A.
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KALOS M D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.0%;
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43.7%;
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43.
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amino acid
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SEQ ID NO 176.
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      Score 426.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
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Pred. No. 4.5e-25;
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    426.5; DB 4
No. 4.5e-25;
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No. 4.5e-25;
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No. 4.5e-25;
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Best Local Similarity
RESULT 1446
ID AAB31579 standard; p
DE Amino acid sequence
PN W0200078332-A2.
PD 28-DEC-2000.
                                                                                                                                  Best Local Similarity RESULT 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1445
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RESULT 1444
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RESULT 1442
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RESULT 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JULY 1443
ABB09589 standard; process., -
Deinagkistrodon acutus venom thrombin-11xe
CN1181421-A.
) 13-MAY-1998.
13-MAY-1998.
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14-MAY-1998.
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Prostate tumour protein #
US2002081580-A1.
27-JUN-2002.
(XUJJ/) XU J.
(DILL/) DILLON D C.
                                                                   G-coupled protein WO200283841-A2.
                                                                                                                                                                                                                                                                                                                                                                                Human protein; modification a wo2003031939-A2.
17-APR-2003.
                                                                                   ADE15982 standard; protein; G-coupled protein receptor r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptide SeqID9039. W0200216439-A2. 28-FER->^^
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                             (CURA-)
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Human prostate specific prot
                                                                                                                                                                                              BJAR/) BJARNASON J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-2003
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                          CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                        INCYTE GENOMICS INC. h 30.7%; Similarity 37.8%;
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                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                           peptide; 225 AA.
e of cod trypsin
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                                                                                                                                                                                              B
                                                                                                                                                    30.6%;
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    30.6%;
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43.7%;
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protein
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                                                                                     related
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m thrombin-like
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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1 P703P-DE13.
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  420;
                                                                                     polypeptide,
                                                                                                                                                                                                                                                                                                                            422; DB 6;
No. 1.1e-24;
                                                                                                                                                  421; DB 4;
No. 1.3e-24;
                                                                                                                                                                                                                                                             isozymes
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No. 1.3e-24;
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No. 4.5e-25;
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No. 4.5e-25;
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No. 4.5e-25;
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1e-24;
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e-25;
  7;
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DB 5;
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  218;
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LOCAL SIMILARITY

RESULT 1453

ID ADA05736 stand*
PN W02030^
PD 10-
PA
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Best I
RESULT
ID AP
DE H
PN W
PD (
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Best Local Similarity
RESULT 1449
ID AAY28641 standard; p
DE Human secreted prote
PN W09940183-A1.
PD 12-AUG-1999.
PA (HUMA) HUMAN GENOME
                                                                                                                                                                                                                                                              Query Match
Best Local S
RESULT 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESUL RESULTANT RESULT
                              Human NOV18c protein; BQ ID W02003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW46773 standard; protein; 233 AA.
Amino acid sequence of Salmonase.
EP814164-A2.
29-DEC-1997.
(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
DET MACCH 30.4%; Score 41
Local Similarity 36.6%; Pred. No
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(HUMA-) HUMAN GENOME SCI INC.

30.4%;

31Y Match 30.4%;

46.1%;
                                                                                                                                                                                 Trypsin domain consensus US2002165152-A1. 07-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                            Human trypsin d
WO200226802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28641 standard; protein;
Human secreted protein from
WO9940183-A1.
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                                                                                                                                                                                                                                            ABG75786 standard; protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                       AAE21442 standard;
                                                                                                                                                                                                                                                                                                                                              04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL93921 standard; protein;
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US2004006205-A1.
                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC.
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                                                                                                                                                                KAPE/) KAPELLER-LIBERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                 Local Similarity
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BURGESS C E.
MALYANKAR U M.
SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GERLACH V
LIU X.
MILLER C
SPYTEK K
ZERHUSEN
PENA C E
SHENOY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHSON G.
CASMAN S J.
BOLDOG F L.
VOSS E Z.
VERNET C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZHONG M.
MEZES P S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAZUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHONG H.
SMITHSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAUPIER R J. EDINGER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACDOUGALL J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RASTELLI L.
ANDERSON D
                                                                                                                                                                                                                                                                                                                                                                                dard; protein; 226 AA.
domain consensus protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein receptor-related protein #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G № B № B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ε
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽.
                                                                                                                        30.3%;
                                                                                                                                                                                                                                                                                 30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                       веquence,
                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA.
cDNA clone
                                                                   198 AA.
NO:96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                            Score 416.5; DB 6;
Pred. No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                          Pred.
                                                                                                                                                                                                                                              A
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No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       417.5; DB 2;
No. 2.5e-24;
                                                                                                                                                                                                                                                                                   416.5; DB 5;
No. 2.9e-24;
                                                                                                                                                                                                                            SMART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                  #2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 233;
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218;
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Query Match
Best Local S
RESULT 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
RESULT 1454
                                   Query Match
Best Local Similarity
RESULT 1458
                                                                                                Query Match
Best Local Similarity
RESULT 1457
                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                            Query Macch
                                                                   Human diagnostic and therape WO2004023973-A2.
                                                                                                                               Human protein modification a WO2003083084-A2.
                                                                                                                                                                                           ADA50560 standard; protein; 194 AA. prostate specific antigen (PSA/KLK3), WO200303159-A2.
            ABM83248 standard;
Human diagnostic as
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NOV18c.
US2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN62900
                                                           (INCY-) INCYTE
                                                                                                                                                                                   (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                 (ANDE/
                                                                                                                                                                                                                                                                                                                                                                                                                                             (PATT,
                                                                                                                                                                                                                                               GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                              AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                    RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M I
                                                                                                                                                                                                                                                                                                                                                                                                                                     PATTURAJAN N
SPYTEK K A.
EDINGER S R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                       INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                 GORMAN L.
ZERHUSEN B
ANDERSON D
ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TI I.
                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                         EISEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                      ELLERMAN K.
MALYANKAR U M.
INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                          CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                     d; protein; 299 A and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>بر</del>
                                                                                                                                                                                                                                                                                                                                                                                         ₹ 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                 30.0%;
                                           29.8%;
37.1%;
                                                                                                       29.8%;
37.1%;
                                                                                                                                                                    29.8%;
                                                                                rotein; 215 AA.
therapeutic pprotein
                                                                                                                                                                                                                                                                                                              M
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                                                                                                                                               and
                                                                                                                                                      215
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                             299 AA.
                                                                                                       Score
Pred.
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Pred.
                                                                                                                                                                                                                                Score
Pred.
                                            Score 409; DB 8;
Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 412.5; DB 6
Pred. No. 5.2e-24;
                                                                                                                                               maintenance molecule
                                                                                                                                                      A
                     pprotein
                                                                                                                                                                    409;
No. 9.
                                                                                                         409;
No. 1.
                                                                                                                                                                                                                                 412.5; DB 8;
No. 5.2e-24;
                                                                                                                                                                                                          SEQ ID
                                                                                                         DB 7;
.1e-23;
                                                                                                                                                                     DB 6;
.5e-24;
                      SEQ
                                                                                  SEQ
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                      ä
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                                                  Length 215;
                                                                                                                                                                           Length
                      NO:3497
                                                                                  NO:3078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 198;
                                                                                                                                                                                                                                         Length
                                                                                                                                             polypeptide
                                                                                                                                               SeqID8
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Query Match
Best Local Similarity
RESULT 1463
                                                                                                           Best Local Similarity RESULT 1462
                                                                                                                                                                            Best Local Similarity RESULT 1461
                                                                                                                                                                                                           Best
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BESULT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                      AAW76538 standard; protein;
A. contortrix protein C acti
                                                                                AAB08510 standard; pro
A recombinant protein
WO200050612-A2.
                WO9842850-A1.
                                AAW76538 standard;
                                                                                                                                                  ABM82641 standard; protein; 222 A Human diagnostic and therapeutic WO2004023973-A2.
  (RPMS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIT/) SMITHSON G.
(MILL/) MILLET I.
(PEYM/) PEYMAN J A.
(KEKU/) KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADN62902 standard; protein; Human NOV18d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV18d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA05738 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
1460
                                                                                                                                                                                               ) EISEN A.
) GANGOLLI E A.
) RIEGER D K.
) SPADERNA S K.
                                               INSTRUMENTATION LAB.

th 29.6%;
Similarity 36.2%;
                                                                                                                                                                                                                                AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                          PENA C E A.
SHENOY S G.
SHIMKETS R A
ROTHENBERG M
LEACH M D.
RPMS TECHNOLOGY LTD
                                                                                                                                 INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                            ELLERMAN K.
MALYANKAR U M.
ORT T.
                                                                                                                                                                                                                                                                                                                                                GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                          MILLER C E.
RASTELLI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                      10 j.
                                                                                                                                                                                                                                                                                                   STONE D J.
                                                                                                                                                                                                                                                                                                                                   CATTERTON E.
                                                                                                                                                                                                                                                                                                                                            ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                   EDINGER S
                                                                                                                                                                                                                                                                                                                                                                                                            SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                     PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ndard; protein;
protein SEQ ID
                                                                                        protein; 230 A/
in C activator
                                                                                                                                                                                                                                                                   3 >
                                                                                                                 29.6%;
36.7%;
                                                                                                                                                                                  29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
                     ein; 231 AA.
activator protein
                                               Score
Pred.
                                                                                                                 Score
Pred.
                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AA.
NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 409;
Pred. No. 1
                                                                                                 A
                                                                                                                                                        pprotein
                                                                                        polypeptide
                                               406
No.
                                                                                                                407;
No. 1.
                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408.5; DB 6;
No. 9.6e-24;
                                                .5; DB 3;
1.8e-23;
                                                                                                                                                                                 .5; DB 8;
9.6e-24;
                                                                                                                DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                     fragment
                                                                                                                                                        SEQ ID
                                                                                                                8;
-23;
                                                                                                                        Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 299;
                                                                                                                                                        NO:2890.
                                                                                                                                                                                      Length
                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                       230;
                                                                                                                                                                                        181;
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Best Local Similarity
RESULT 1472
ID AAM52946 standard; p
DE Batroxobin, a snake
PN KR98002267-A.
PD 30-MAR-1998.
                                                                                                                 Query Match
Best Local Similarity
RESULT 1471
ID AAE21441 standard; p
DE Human trypsin domain
PN W0200226802-A2.
PD 04-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
RESULT 1464
ID ABB09590
DE Deinagkis
                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1470
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
RESULT 1465
                                                                                             Query Match
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                              AAM52946 standard; patroxobin, a snake
                                                                                                                                                                                                                                                                                                          Batroxobin gene product.
JP02124092-A.
11-MAY-1000
                                                                                                                                                                         (BRIM ) BRISTOL-MYERS SQUIBB ry Match 29.3%; Local Similarity 32.9%;
                                                                                                                                                                                                                        WO9929838-A1.
                                                                                                                                                                                                                                    Araraca batroxobin
                                                                                                                                                                                                                                               AAY17869 standard;
                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1988.
(YAMA/) YAMASHINA
                                                                                                                                                                                                                                                                                                                                                                                                          JP63049084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR20557 standard; protein; Fibrinogenolytic protein #4 DE4023699-A.
                                                                                                       (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                             (FUJI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM84665 standard;
Human diagnostic ar
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INITIAL OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP81333 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200050612-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB08511 standard; protein; 230 AA.
Biosynthetic variant of protein C a
                                                                                                                                                                                                             7-JUN-1999
                                                                                                                                                                                                                                                                                                        11-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INLI ) INSTRUMENTATION LAB.
ry Match 29.4%;
t Local Similarity 37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinagkistrodon CN1181421-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB09590 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BADI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE CORP
    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
MOKAM BIOTECHNOLOGY RES INST.
h 29.1%; Score 400;
                                                                                                                                                                                                                                                                 FUJISAWA PHARM CO L'h 29.3%;
Similarity 32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASF AG.
                                                                                                                                     dard; protein; 249 AA.
domain consensus prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acutus venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d; protein; 220 AA.
and therapeutic pprotein
                                                                                                                                                                                                                                                                                                                                                                                    H.
                                              protein; 231 AA.
e venom protease.
                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                29.2%;
                                                                                                                                                                                                                                                                                                                                                             29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.3%;
36.7%;
                                                                                                                                        consensus protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.5%;
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                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                              255 AA
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                                                                                Score
Pred.
                                                                                                                                                                          CO.
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from snake venom
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m thrombin-like
                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 1.8
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                                                                                401
No.
                                                                                                                                                                          402;
No. 4
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No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activator
                                                                                                                                                                                                                                                                                                                                                            402;
No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      403; DB 2;
No. 3.3e-23;
                                                                               .5; DB 5;
4.6e-23;
                                                                                                                                                                          4.3e-23;
                                                                                                                                                                                                                                                                   ; DB 2;
4.3e-23;
                                                                                                                                                                                                                                                                                                                                                            1.3e-23;
                                                                                                                                        #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5; DB
3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAD SCI.
5; DB 5;
2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8e-23;
  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
.2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
  2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
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Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (218
                                                                                                                                                                                                                                                                                                                                                                        255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue variant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230;
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worked by the standard of the 
                                                                                                                                                 RESULT
ID AA
DE P1
PN JP
PD 06
PA (S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ыевt Local Similarity
RESULT 1474
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse serine pr
WO200031243-A1.
                                                                                                                                                                               AAP70758 standard; protein; Pig pancreas elastase-2. JP62000276-A.
                                                                                                                                                                                                                                                                                                                                       ADE58223 standard; protein; ihuman Protein P00746, SEQ ID W02003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG75785 standard; protein; 227 AA. Trypsin domain consensus sequence, US2002165152-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flaboxobin, a snake KR98002267-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11711 standard; protein; Mouse serine protease BSSP5
                                                                               AAE39992 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE39993 standard; protein;
Human adipsin protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM52945 standard;
                                               Human adipsin protein
US2003092620-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM82831 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOKA-) MOKAM BIOTECHNOLOGY
Y Match 28.7%;
Local Similarity 36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FUSO ) FUSO PHARM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                       KAPE/) KAPELLER-LIBERMANN
                                                                                                                                                                                                                                    Local Similarity
1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                       GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; protein; 233 A and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                   LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
rotein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 236 AA
e venom protease
                                                                                                              28.2%;
38.5%;
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39.1%;
                                                                                                                                                                                                                                                                                                     CORP.
                                                                                                                                                                                                                                                                                                                                                                                                      28.3%;
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38.5%;
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37.3%;
28
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. 2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 394;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                      253 AA.
D NO 4094.
                                                                                253
                                                                                                                                                                                                                      269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA.
from snake venom.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (mBSSP5)
                                                                                                              Score
Pred.
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Pred.
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Pred.
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Pred.
Score
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pprotein
                                                                                                                                                                                                                                                                                                                                                                                                         389;
No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391;
No. 3
387;
                                                                                                                                                                                                                                                      389;
                                                                                                                  388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395.5; DB 3;
No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392; DB 8;
No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393; DB 2
No. 2e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; DB 2;
1.7e-22;
                                                                                                                                                                                                                                                    ; DB 7;
4.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                         w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 7
3e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
1.9e-22;
                                                                                                                  DB 1;
.5e-22;
B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                       253;
                                                                                                                                                                                                                                                                                                                                                                                                                         227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236;
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Best Local Similarity
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1488
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1483
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                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                             ABR39439 standard; I
Human GENSET polypeI
WO2003014151-A2.
20-FEB-2003.
                                                                                                                                            (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                              (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
                                                                                                                                                                                                                                                                                                                                                                               ABM82644 standard; protein; 212 AA. Human diagnostic and therapeutic pprotein WO2004023973-A2.
                                                                                                                                                                                                           ADR66037 standard; protein; 213 AA Human prostatic carcinoma derived | WO2004076614-A2.
                                                                                                                                                                                                                                                                                             Tumour-associated WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB11710 standard; protein;
Human serine protease BSSP5
                                                                               WO2004076614-A2.
                                                                                          ADR66935 standard; protein; 213 AA
Human prostatic carcinoma derived |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus sequence WO2003031463-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200031243-A1.
                                                                                                                                                                                                                                                                                                                  ABM81778 standard;
                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM82830 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU09382 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FUSO ) FUSO PHARM
                                                                                                                                                                              (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE CORP.
Local Similarity
                   PILARSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                             INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ndard; protein; 264
polypeptide clone n
                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                      ; protein; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 IND LTD.
28.1%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 271 AA.
of trypsin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 212 AA.
nd therapeutic pprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%;
40
                                                                                                                         28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.1%;
36.8%;
                                                                                                                                                                                                                                                                                                                                      28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.5%;
                                                                                                                                                                                                                                                                                                     264 AA.
target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 AA.
(hBSSP5)
 Score
Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AA.
name
                                                                                            DNA
                                                                                                                         385;
No. 7.
                                                                                                                                                                                                                      protein
385;
No. 7.
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No. 7e-
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No.
                                                                                                                                                                                                                                                                                                        (TAT)
                                                                                                                                                                                                                                                                                                                                       385.5; DB 8;
No. 6.7e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vCTRL-1
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                                                                                            SEQ ID 233
                                                                                                                                                                                                                                                                                                                                                                                                                        6.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7e-22;
                                                                                                                                                                                                                                                      ထ ပ်္ပ
 DB 8;
                                                                                                                                                                                                                                                     ).4e-22;
                                                                                                                         DB 8;
.4e-22;
                                                                                                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
,-22;
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                                                                                                                                                                                                                      SEQ ID
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                                                                                                                                                                                                                                                                                                        PRO2719,
                                                                                                                                     213;
                                                                                                                                                                                                                                                                                                                                                 212;
                                                                                                                                                                                                                                                                                                        SEQ: 4580.
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Query Match
27.8%; Score 38
Best Local Similarity 37.2%; Pred. No
RESULT 1497
ID AAR05421 standard; protein; 250 AA.
DE Human adipsin/D encoded by a cDNA.
PN W09001540-A.
PD 22-FEB-1990.
PA (CALB-) CALIF BIOTECHN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1493
ID AAU79393 standard; p
DE Novel human kallikre
PN W0200214485-A2.
PD 21-FEB-2002.
                                                Best Local Similarity RESULT 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1490
ID AAP6172
DE Porcine
PN JP61192
PD 26-AUG-
PA (KIRI)
                                                                                                                                                                                                           DE PN PA PA PA PA
                                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 1495
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Best Local Similarity
RESULT 1494
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                                                                           Query Match
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08_APR-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
27.8%;
ery Match 27.8%;
35.8%;
ADE59221 standard; protein; 263 AA.
Rat Protein AAB31922, SEQ ID NO 4092.
WO2003016475-A2.
                                                   (CALB-) CALIF BIOTECHN INC.
(CALB-) CALIF BIOTECHN 27.8%;
iry Match 27.8%;
                                                                                                                                                                                                                                                                                                                                                           ABM82642 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein
W02004023973-A2.
25-MAR-2004.
(INCY) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1990.
(BADI ) BASF AG.
(BACH/) BACH A.
                                                                                                                                                                     (BETH-) BETH ISRAEL HOSPITAL ASSOC.
(DANA-PARBER CANCER INST.
(META-) METABOLIC BIOSYSTEMS INC.
(BETH-) BETH ISRAEL HOSPITAL ASSOC.

ry Match
27.8%; Score 382;
t Local Similarity 37.2%; Pred. No. 1.
                                                                                                                                                                                                                                                                            AAR05772 standard; protein; 250 AA. Human adipsin gene product from the clone W09006365-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN10933 standard; protein; 171 AA. Human kallikrein 15, marker of endocrine WO2004029285-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU79393 standard; protein; 171 AA.
Novel human kallikrein KLK15, splice variant #3.
WO20021448-A2.
21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 27.8%;
t Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snake venom ancrod WO9006362-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine elastase JP61192289-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR05775 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO INC. (KNOL ) KNOLL AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP61724 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KIRI ) KIRIN BREWERY KK.

cy Match 27.9%;

c Local Similarity 38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6-AUG-1986.
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 272 AA. polypeptide.
                                                                                                                                                                                                                                                                                                                                   27.8%;
35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%;
                                                         Score 382;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 382.5; DB 8;
Pred. No. 9.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 383; DB 2;
Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                   382;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382.5; DB 5;
No. 9.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383; DB 2;
No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384; DB 1;
No. 1.1e-21;
                                                         DB 2;
.5e-21;
                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                   DB 8;
.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer
                                                                                                                                                                                                                                                                                          phg31
                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                    Length
                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                          NO:2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272;
```

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Query Match
Best Local Similarity
RESULT 1499
ID ADN99596 standard; p
DE Novel human protein
                                                                               SULT 1499
SULT 1499
ADN99506 standard; protein,
E Novel human protein sequence #412.
N W02004038003-A2.
PD 06-MAY-2004.
PD 06-MAY-2004.
PA (FIVE) FIVE PRIME THERAPEUTICS INC.
27.6%; Score 379.5; DB 8; Le
PA (FIVE) FIVE PRIME THERAPEUTICS INC.
27.6%; Pred. No. 1.7e-21;
                                                                                                              Best Local Similarity RESULT 1500
   Best Local Similarity
                                                                                                                                             Query Match
                                                         ABU92049 standard; protein; 220 AA.
Human protein modification and maintenance molecule-29 (PMM-29)
W02003031939-A2.
                                                                                                                                                                                                                                                                                27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                   17-APR-2003.
INCYTE GENOMICS INC. h 27.6%; Similarity 37.2%;
                                                                                                                                                                                                                                                   27.7%;
37.6%;
   Score
Pred.
                                                                                                                                                                                                                                                     Score 381;
Pred. No. 1.
 379;
No. 2.
                                                                                                                                                                                                                                                       DB 7;
.9e-21;
   DB
2e
 -6;
-21;
              Length 220;
                                                                                                                                                                                                                                                                  Length
                                                                                                                                          Length 187;
```